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Search completed: Octobe
Job time: 62.3343 secs
                                                                                                                                       Query Match
                                                                                                                                                                Best Local
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                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                           04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 FRHH--ETSGDLATEYLQLMV--YVTK----TSIKIPSSHTLMKGGSTKYWSGNSEFHFY 273
                                                                                                                     244 LEGAETUTPYVDPIGYGSLW-----YTSVGFGGLAQLRSGERVYVNISHPDMVDYRRG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 QPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
---SNGKLIVNQDGFYYLYANICFR-HHETSGDLATEYLQL--MVYVTKTSIKIPSSHTL 255
                                                                                          256 MKGGST------KYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245 C;Comment: This protein is an important proximal mediator of endotoxemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X62141; NID:938159; PIDN:CAA44068.1; PID:938160
                                             185 FSPTHG-LALPQDGVYYLYCHVGYRGRTPPAGRSRARSLTLRSALYRAGGAYGRGSPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; ilpoprotein; myristylation; transmembrane
F; 19, 20/Binding site: myristate (Lys) (covalent) *status predicted
F; 81, Päinding site: carbohydrate (Ser) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sednences
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                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor alpha precursor - baboon
C.Species: Papio sp. (baboon)
Tate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 FKGGGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          K;Sanjanwala, M.; Edwards, A.
submitted to the EMEL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from
A;Reference number: S22052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 SINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor alpha precursor - horse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Equus caballus (domes C; Date: 10-Sep1999 #sequence_re C; Accession: JQ1344 R;Su, X.; Morris, D.D.; McGraw, Gene 107, 319-321, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: TNF-alpha
A; Introns: 62/3; 79/1; 95/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comment: This protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 62/3; 78/1; 94/1
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-233 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: I-234 <SUX>
                                                                                                                                                                                                                                      297 KTFFGAVMV 305
                                                                                                                                                                                         305 ATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ccession: S22052
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tumor necrosis factor alpha precursor - bovine
C:Species: Bos primidentus taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: 146047; S24642
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin an A;Reference number: 146046; MUID:94083525
A;Accession: 146047
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-233 <CL2>
C; Superfamily: tumor necrosis factor
C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;
F;78-234/Product: tumor necrosis factor alpha *status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) *status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) *status predicted
F;146-178/Disulfide bonds: *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 Y-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYOGGVFOLEKGDRLSAEIN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 VIGPOREESPGGPSINSPLVQTLRSSSQASSNRPVAHV---VADINSPGQL----- 102
                                                                                                                                                                                                                                                                                                                                                                                                                191 RGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH--------ETSGDLATE 234
                                                                                                                                                                                                                                                                                                                                                                     163 QPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANIC 221
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 YLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:214137; NID:9796; PIDN:CAA78511.1; PID:9798 C;Genetics:
A;Gene: TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 62/3; 78/1; 94/1
C; Superfamily: tumor necrosis factor
C; Keywords: 91ycoprotein; lipoprotein; myristylation; transmembrane
F; 20/Binding site: myristate (Lys) (covalent) #status predicted
F; 81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 81/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                  7.6%; Score 128; DB 1; Length 234; 24.2%; Pred. No. 0.0026; Live 32; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --YEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 7.5%; Score 126.5; DB 1; Best Local Similarity 25.5%; Pred. No. 0.0035; Matches 50; Conservative 25; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 FRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--
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                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                Similarity
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October 10, 2002, 15:59:11

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M.B.; Kozlov, S.V.; No
endotoxin
                                                                                                                                   macrophage;
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A;Accession: I49076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 149139; 149138; 149076
F;Lauton, P.; Nelson, J.; Tizard, R.; Browning, J.L.
J. Immunol. 154, 239-246, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-306 <-RE3>
A,Cross-references: EMBL:U16984; NID:g577431; PIDN:AAB60493.1; PID:g577432
B,Pchholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov
Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995
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  in response to
                                                                                                                                                                                                                                                                                                                                                                                                                        163 OPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNODGFYYLYANI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 CFRHHETSGDLATEYLQLMVYVTK------TSIKIPSSHTLMKGGSTKYWSGNS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESQDTKLIP----DSCRRIKQAFQGAVQKELQHIVGSQHIRAERAMVDGSWLDLAKRSKLE 161
                                                                    A.Introns: 62/3; 81/1; 97/1
C.Superfamily: tumor necrosis factor
C.Superfamily: tumor necrosis factor
F.Reywords: cytokine; cytotoxis; alycoprotein; lipoprotein; lymphokine;
F.80-235/Product; tumor necrosis factor #status predicted <a href="MAR">MART></a>
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:148-179/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 AQPFAHLTIN--ATDIPSGSHKVSLS-----SWYHDRG--WAKISNMTF----
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     macrophages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YEPMYLGGVFQLEKGDLLSAEVNLPKYLDITESGQVYFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Till: Characterization of the mouse lymphotoxin-beta A;Reference number: 149138; MUID:95088371 A;Accession: 149139
                                                                                                                                                                                                                                                                                                                                ,0013;
, 59;
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Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                      25.38; Pred. ....
  ρλ
                                                                                                                                                                                                                                                                                                                     7.8%; Score 131.5;
25.3%; Pred. No. 0.0
  C;Comment: Tumor necrosis factor is secreted C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-306 <RES>
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.3%
Matches 41; Conservative
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nes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-306 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: LT-beta
A; Introns: 54/3; 160/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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Matches
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A; Residues: 1.235 < CWOO.
A; Cross-references: GB:L00981; NID:9205253; PIDN:AAA16275.1; PID:9205254
A; Cross-references: Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. HOPPe-Seyler 373, 271-281, 1992
A; Fitle: Rat tumor necrosis factor-alpha Transcription in rat Kupffer cells and in
A; Reference number: S21674; MUID:92329007
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A; Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
A; Cross-references: GB:X66539; GB:S40199; NID:9395369; PIDN:CAA47146.1; PID:9395370
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N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Species: O7-Jun-1990 *sequence_revision O7-Jun-1990 *text_change O4-Feb-2000
Accession: JU0029; JN0868; S21674
                                                                                                                                         tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 YANICFRHHETSGDLATEYLQLMVYVTK-----TSIKIPSSHTLMKGGSTKYW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 KPVAHVVAN------HQVDEQLEWLSRG----ANALLANGMDLKDNQLVIPADGLYLV 137
                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                            :Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
                                                                                                                                                                                                          C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene
A;Reference number: I54490; MUID:92218012
A;Accession: I54490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
predicted
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25.3%; Pred. No. 0.0011;
tive 27; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 QPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli
          PIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFG 229
                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: DNA
A.Residues: 1-235 CSHI.
A.R.Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A.Fitle: Cloning and sequence analysis of
A.Reference number: JN0868; WUID:94040766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.3%
Matches 42; Conservative
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A; Residues: 1-235 <RES>
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A; Molecule type: protein A; Residues: 77-99 <TAK>
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A; Residues: 1-233 <IRI>
A; Residues: 1-233 <IRI>
A; Residues: 1-233 <IRI>
A; Cross-references: ERBL:215026; NID:g37211; PIDN:CAA78745.1; PID:g37212
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
B; Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature: 312, 724-729, 1984
A; Title: Human tumour necrosis factor: precursor structure, expression and homology to 1
A; Reference number: A93351; MUID:85086244
A; Reference number: A93351
A; Molecule type: MRNA
A; Residues: 1-233 <PEN>
A; Residues: 1-233 <PEN>
A; Residues: 1-233 <PEN>
A; Ross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
A; Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelc R; Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.; Science 228, 149-154, 1985
A; Title: Wolecular cloning of the complementary DNA for human tumor necrosis factor.
A; Reserence number: A44189; MUID:85142190
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C:Dsecies: Home saplens (man)
C:Dsecies: Home saplens (man)
C:Dsecies: Home saplens (man)
C:Date: 28-Aug-1965 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R:Nedwin, G.E.; Naylor, S.L.; Sakaguchl, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 631-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chrc
A;Reference number: A93585; MUD:86016093
A;Residue type: DNA
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R.Ixis, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
Reference number: S36152; MUID:93272029
C; Reywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lymphd 17.17/Domain: propeptide $status predicted <PRO. F; 78-234/Product: tumor necrosis factor alpha $status predicted <TUM> F; 20/Binding site: myristate (Lys) (covalent) $status predicted <TUM> F; 20/Binding site: myristate (Ser) (covalent) $status predicted F; 96/Binding site: carbohydrate (Ser) (covalent) $status predicted F; 96/Binding site: carbohydrate (Asn) (covalent) $status predicted F; 96/Binding site: sarbohydrate (Asn) (covalent) $status predicted
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A; Residues: 1-62,'s', 64-233 <MAN>
A; Cross-references: GB:M10968; NID:g339737; PIDN:AAA61198.1; PID:g339738
A; Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
R; Fukuda, S:; Ando, S:; Sanou, O:; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;
Lymphokine Res. 7, 175-185, 1988
                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 IVGSQHIRAEKAMVDGSW---LDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ISAP 100
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                                                                                                                                                                                                                                                                                                                 Length 234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor alpha precursor [validated] - human N;Alternate names: cachectin; TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VIGPQ--REEGSPAGPSFNRPLVQTLRSSSQASNNRPVAHVVAN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 YHDRGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-
                                                                                                                                                                                                                                                                                                         8.1%; Score 137; DB 1;
26.1%; Pred. No. 0.00046;
tive 30; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 EVSNPSLLD-PDQDATYFG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EINLPEYLDYAESGOVYFG 230
                                                                                                                                                                                                                                                                                                                                                     Similarity 26.1%;
52; Conservative 3
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Best Local S:
Matches 52
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Afross-references: GB:S68530; NID:9544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific A;Reference number: A59163; MUID:93018820
A;Title: Myristyl acylation of myristylated lysines
A;Contents: annotation; identification of myristylated lysines
B;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; B
J. Blol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization A;Reference number: A92511; MUID:85130974
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc out detriment to normal cells. It can also act synergistically with interferon gamma C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clc ut are produced by different cell types and have different induction kinetics.
                                                                                                                                                                A, Molecule type: protein
A;Residues: 83-102;109-119;121-128, X, 130-131;142-144, X, 146, XXX, 150-152;159-174
A;Residues: 83-102;109-119;121-128, X, 130-131;142-144, X, 146, XXX, 150-152;159-174
B;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashi Eur. J. Blochem: 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparing A;Reference number: 153311; MUID: 86030296
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta A;Reference number: A61478; MUID:88301617
A;Accession: B61478
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C; Keywords: cytokine; cytokoxin; alycoprotein; homotrimer; lipoprotein; lymphokine;
E1.7 (Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
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Immunogenetics 39, 150-184, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter
A;Reference number: 154522; MUID:94102009
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F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F:145-177/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-233 <MAR>
A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Experimental source: U-937 cells ; Fakakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, ur. J. Biochem. 235, 431-437, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:120441; OMIM:191160
A; Map position: 6p21.3-6p21.3
A; Introns: 62/3; 78/1; 94/1
C; Complex: homofrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: translated from GB/EMBL/DDBJ
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13;

Gaps

9

201

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A;Title: Sequence of the cDNA encoding owine tumor necrosis factor-alpha: problems wi A;Title: Sequence of the cDNA encoding owine tumor necrosis factor-alpha: problems wi A;Reference number: JH0529; MUID:92112044
A;Reference number: JH0529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404.
A;Note: comparison with the introns of homologous sequences suggest that this is prot
C;Superfamily: tumor necrosis factor
                        C; Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; P;1-81, Domain: propeptide *status predicted <PRO>P;1-81, Domain: propeptide *status predicted <PRO>P;82-234/Product: tumor necrosis factor *status predicted <PAMT>P;92-234/Products: tumor necrosis factor *status predicted <PRO*Pisson *status predicted P: *sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of ovine TNF-alpha
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: JH0529; S48118; S13114; S20661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKG--- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAA40076.1; PID:g297807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406 A;Experimental source: alveolar macrophage R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E. Immunol. Cell Biol. 69, 273-283, 1991 A;Title: Molecular cloning, expression and characterization of ovine TN A;Reference number: $48118; MoID:92155784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 EKAMYDGSWLDEAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN-MTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TDNQLVVPADGLYLIYSQVLF----SQGCRSYVLLTHTVSRFAVSYPNKVNLLSAIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 EGPLHAPPPPAPHQPPAASR---: SMFVALLGLGLGLGQVVCSVALFFYFRAQMDPNRISED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 BGPL----PKKAGGPQGSKRCLCLSLFSFLLVAGAÄÜLFC----LLHFRVIGPQEBESPN
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                                                                                                                                                                                                                                                                                                                 Length 234;
                                                                                                                                                                                                                                                                                                                 8.4%; Score 141; DB 1;
21.6%; Pred. No. 0.00021;
tive 35; Mismatches 99
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    sheep

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Nucleic Acids Res. 18, 6723, 1990
A;Title: Primary structure of ovin
                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%
Best Local Similarity 21.6%
Matches 65; Conservative
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A; Residues: 1-62,64-234 <YOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-234 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-234 <NAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
Molecule type: mRNA
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Nighternate names: cachectin; TWF alpha
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Saccession: A22454; A25451; J50727
R; Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
Bh A5, 1494-156, 1986
A; Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rab eference number: A25454; MUID:86219711
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A; Residues: 1-234 <1T2>
A; Residues: 1-234 <1T2>
A; Residues: 1-234 <1T2>
A; Residues: 1-231 <1T2>
A; Residues: 1-221, 1990
Gene 95, 215-221, 1990
A; Reference number: JH0309; MUID: 91065534
A; Recession: JS0727
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A; Residues: 1-234 <ITO>
A; Residues: 1-234 <ITO>
A; Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
A; Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
A; Tito, H.; Shirad, T.; Yamamoto, S.; Akira, M.; Rawahara, S.; Todd, C.W.; Wallace, R.B. DNA 5, 157-165, 1986
A; Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A; Reference number: A25451; MUID:86219712
                                                                                                                                                                                                                                                            ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Note: 14,1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;80-235/Product: tumor necrosis factor #status experimental -AMAT>
F;80-235/Product: tumor necrosis factor #status experimental -AMAT>
F;80-235/Product: tumor necrosis factor #status experimental -AMAT>
F;80-235/Product: carbohydrate (Ser) (covalent) #status predicted
F;80-235/Production = factor #status predicted
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-230, "K', 232-235 < REES>
A; Residues: 1-230, "K', 232-235 < REES>
A; Residues: 1-230, "M', Zentella, "Cerami, A: Cerami, A: Cerami, A: Gentella, A: Cerami, A: Cerami, A: Gentella, A: Cerami, A: Michem. Blophys. Res. Commun. 173, 1072-1078, 1990
A; Title: Characterization of high molecular weight glycosylated forms of murine tumor. A; Reference number: A36696; MUID:91097531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 QPFAHLTINATDIPSGSHKVSLS-SWYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 LFK-----GOGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW---- 192
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Pred. No. 0.00019;
8; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFHFYSINVGGFFKLRSGEEISIEVSNPSLLD-PDQDATYFG 309
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25.9%; Pre
tive 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 CFRHHETSGDLATEYLQLMVYVTK-
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                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 80-85,'X',87-99 <SHE>
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A; Residues: 1-62, 'Q', 63-234
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A; Cross-references: GB:M603.
C; Genetics: 62/3; 80/1; 96/1
A; Introns: 62/3; 80/1; 96/1
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change 04-Feb-2000

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A) Residues: 1.235 FFRA.
A) Residues: 1.235 FFRA.
A) Cross-references: GB:X02611; NID:954844; PIDN:CAA26457.1; PID:954845
R) CSCH, K.; Beutler, B.
Bitler, R.; Beutler, B.
A) Fittle: Alternative cleavage of the cachectin/tumor necrosis factor propeptide result, Reference number: A34251; MUID:89380231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA 7, 193-201, 1988
A;ittle: Clonhing and expression in Escherichia coli of the gene for mouse tumor necr
A;Reference number: A22908; MUID:88224564
A;Accession: A22908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Identification of a common nucleotide sequence in the 3'-untranslated regio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087; Note: article in Russian with English abstract; Samon, D:; Rawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A. ucleic Acids Res. 15, 9083-9084, 1987
Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor; Reference number: A93679; MUID:88067722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Shakhov, A.N.; Nedospasov, S.A.
Bioorg, Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete
A;Reference number: S03791; MUD:87298639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stross references: GB:Y00467; NID:954830; PIDN:CAA68530.1; PID:954832; Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V. Coc, Natl. Acad. Sci. 0.5A. 82, 6060-6064, 1985
Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor; Reference number: A25164; MUID:85298296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.; Beutler, B.; Hartog, R.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A. tl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
                                                             120 PQIAAHVISEAS----SKTTSVLQW-AEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYA 173
                                                                                                                                  NICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
                                                                                                                                                                              174 QVTFCSNREASSQAP-----FIASLCLKSPGRFERILLRAANTH--SSARPGGQOSIH 224
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A.; Tavernier, J.; van der Heyden,
AQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 31.Mar-1988 #Sequence_revision 31.Mar-1988 #text_change
C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; ISS
R;Shirai, T; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
                                                                                                                                                                                                                                                                               277 VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                    mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: I59058; MUID:86149365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNF alpha
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N;Alternate names: cachectin;
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A; Residues: 1-235 <SHI>
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Residues: 1-235 <PEN>
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162
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C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C; Accession: S28017; H0793; S26694; S28852; I53476; S25684; S30593
R; Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; BO J. 11, 4313-421, 1992
Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for A; Reference number: S28017; MUID:93049181
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R;Ganchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
FEBS Lett. 315, 259-266, 1993
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A;Reference number: JH0793; MUID:93094757
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A;Residues: 1-261 <GAU>
A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
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Residues: 1-261 <HOL>
Cross-references: EMBL: 215017; NID:g38483; PIDN:CAA78737.1; PID:g38484

Spriggs, M.K.; Armitage, R.J.; Strockbine; L.; Clifford, K.N.; Macduff, B.M.; Sato, Exp. Wed. 176, 1543-1550, 1992
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                                    LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPS 297
                                                                               206 HKVYM--RNFKYPGDLYLMEEKKLNYCT-TGQIWAHSSYLGAVFNLTVADHLYVNISQLS 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --RNLHEDEVEMKTI 69
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A; Molecule type: mRNA
A; Residues: 1-261 <SPR>
A; Cross-references: GB: X67878; NID: 938411; PIDN: CAA48077.1; PID: 938412
A; Experimental source: peripheral blood T-cell
R; Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J: Immunol. 22, 3191-3194, 1992
A; Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A; Reference number: $26694; WUID: 93076854
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LINFEESKTFFGLYKL 278
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A; Residues: 1-261 <GRA>
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J.; Kawashi

DD 46 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999 C;Accession: S53090 C;Accessio
OY 64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF 123	Kimertens, B.E.L.; Murluki, M. submitted to the EMBL Data Library, February 1995 A.Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB. A.Reference number: S53090
OY 124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHK 181	A.Accesion: S53090 A.Status: preliminary A.Molecule type: mRNA A.Residues: 1-261 < MER>
	eferences; EMBL:248469; NID:g732569; PIDN:CAA88363.1; PID:g732570 ttch cal Similarity 24.2%; Pred. No. 2.5e-07;
QY 242 VTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSN 295	Matches 70: Conservative 54; Mismatches 122: Indels 43; Gaps 13; Qy 33 PPPPAPHQPPAASRSMEVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRIL 91
Qy 296 PSLLDPDQDATYFGAFKV 313 : : : : : : :	92 RLHENADPODTTLESODTKLIPDSCRRIKOAFOGAVOKELOHIVGSOHIRAEKAMVDG
RESULT 2 A53062 Fas ligand - mouse	OY 150 SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGK-L 206 13MHKGDQEPQIAAHVISEASSKTTSVLQW-APKGYYTLSNNLVTLENGKQL 161
C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Accession: A33662 R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag	QY, 207 IVNQDGFYYLXANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYW 264
Cell 76, 969-976, 1994 A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A;Reference number: A53062; MUID:94185175 A;Accession: A53062	OY 265 SGNSEPHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDODATYFGAFKV 313
A;Sdatus: preliminary A;Molecule type: mRNA A;Residues: 1-279 < mRN> A;Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565	JLT 4
Query Match 10.9%; Score 184.5; DB 2; Length 279; Best Local Similarity 21.7%; Pred. No. 5.7e-08; Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;	fas ligand - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Accession: A49266
GGGPGAPHEGPLHAPP 	R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S. Cell 75, 1169-1178, 1993 A:Tile: Molecular cloning and expression of the Fas ligand, a novel member of the to A;Reference number: A49266; MUID:94084792
QY 58 GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117	A; Accession: A49266 A; Status: preliminary A; Molecule type: mRNA A; Death diagraph
118 RIKOAFOGAVOKELOHIVGSQHIRAEKANYDGSHLDLAKRSKLEAQPFAHLTINA	A. DESTACES LEGISTRATES (B. 1003470; NID: 9440178; PIDN: AAC52129.1; PID: 9440179 C; Keywords: glycoprotein; transmembrane protein
AELREFTUGSLKVSSFERQIANPSTPSEKREPRSV SWYHDRGWAK ISNWTFSNGKLIVNQDGFYYLYANICFRH	Query Match 10.4%; Score 175.5; DB 2; Length 278; Best Local Similarity 20.3%; Pred. No. 3.3e-07; Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;
Db 151PHSRSIPLEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFRGQSCN 201 Qy 232 ATEXLQLAVYVTKTSIKIPSSHTLAKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI 291	QY 21 GPGAPHEGPLHAPPPPAPAPASRSM
202	OY 58 GOVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117 Db 97 GMYOLFHLOKELAELREFTNHSL-RVSSFFRQIANPSTPSFFKRPRSV 143
258	118 RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPS
RESULT 3 S53090 CD40 ligand - bovine C;Species: Bos primigenius taurus (cattle)	Db 144

09/787,126

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 10, 2002, 12:48:46; Search time 56.3343 Seconds (without alignments) 540.706 Million cell updates/sec

US-09-787-126-2 1685 1 MRRASRDYTKYLRGSEEMGG......LLDPDQDATYFGAFKVRDID 317 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues rched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Si	Description	nemid - bash sea	ligand -	1 ligand -	fas ligand - rat	CD40 ligand - huma	tumor necrosis fac	lymphotoxin-beta -	tumor necrosis fac		tumor necrosis fac		tumor necrosis fac	. tumor necrosis fac	CD40 ligand - mous	tumor necrosis fac	lymphotoxin beta -	collagen alpha 1(I	probable protein k	lymphotoxin alpha	hypothetical prote	TipC protein - sli	probable GntR-fami		gelatinase B (EC 3					
SUMMARIES	ΙĐ	138707	A53062	S53090	A49266	153476	OMMSN	A25451	JH0529	OWHUN	I54490 .	JU0029	149139	S22052	JQ1344	S24642	S12606	S52715	806192	S21738	S11688	A46066	CGHU1S	C84747	OWHUX	S38114	T17414	AC0937	250065	JC1456
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	Query Match Length	281	279	261	278	. 261	235	234	234	233	235	235	306	233	234	233	232	185	193	260	233	244	1464	664	202	450	3848	493	1694	730
	Query Match	11.2	10.9	10.5	10.4	4.6	9.4	8.4	8.1	7.9	7.9	7.8	7.7	7.7	7.6	7.5	7.5	7.4	7.2	7.1	6.9	6.9	8	5.6	5.5	5.5	5.4	5.4	5.4	5.3
	Score	189	184.5	176.5	175.5	158.5	141.5	141	137	133	132.5	131.5	130.5	130	128	126.5	126	125.5	122	120	1117	1117	97.5	94.5	92.5	92.5	91.5	91	90.2	06
	Result No.	-	171	<u>ه</u> ((•	S	9	7	80	6		1	12	13	14	15	16	17	18	19	20	21	22	23	54	22	56	27	28	. 59

homoprotocatechuat	farnesyl-protein t	tumor necrosis fac	glyceraldehyde-3-p	fibrinogen beta ch	probable two-compo	hypothetical prote	probabile phosphoes	leucine-rich repea	heparan sulfate-N-	galactonolactone d	collagen alpha 1(I	protein Pl - Entam	125K surface antig	hypothetical prote	hypothetical prote	• .
AF3526	A47659	B27303	149681.	A25052	C83624	C89893	S51379	T01267	A49733	T06690	CGHU7L	A32935	JH0284	G96722	F72339	
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331	379	202	440	479	639	265	578	684	. 883	. 610	1466	639	1114	1315	279	
5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5. 2.	5.2	5.2	5.2	5.2	ر. ۲.	
89.5	89.5	68	83	89	83	88.5	88.5	88.5	88.5	87.5	87.5	87	87	87	86.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

138707
Fas ligand - human
C;Species: Homo sapiens (man) C:Date: 29-Way-1998 #sequence revision 29-Way-1998 #text change 21-Jul-2000
65; I38554
R; Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 156/-15/4, 1994
A;TILLE: Humman Fas Ilganu: gene structure, chromosommar rocation and species specific A;Reference number: 138707; MOID:95127560
A.Accession: 138707
A;Status; preliminary; translated from GB/EMBL/DDBJ A;Molecule troop mount
A. Mesidues: 1-281 <res></res>
L:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biochem Biochem Biochem Biochem
A.Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A. Reference number: JC2340; MUID:95071350
A, ACCESSION: UC2340
A:Residues: 1-281 <mit></mit>
A; Cross-references: GB: D38122; DDBJ: D29820; NID: 9601892; PIDN: BAA07320.1; PID: 913699
R,Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
Affeterence number: 53/353
A:Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-281 <sch></sch>
K.Alderson, M.K.; Toudgo, T.W.; Davis-Smith, T.; Braddy, S.; Faik, B.; Schooley, K.A. T. Fer Med 181 71-77 1995
A. Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
ı
A;Accession: I38554
A;Status; preliminary; translated from GB/EMBL/DDBJ A.Mologula tune, mbwa
A. Mesidues: 1-281 <re2></re2>
A;Cross-references: EMBL:U08137; NID:9624627; PIDN:AAC50071.1; PID:9624628
C; Genetics:
A)Gene: Fash A:Introns: 151/1: 116/3
C; Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <tmm></tmm>
F;76,184,250,260/Binding site: carbonydrate (Asn) (covalent) #status predicted
11.28;
Best Local Similarity 21.7%; Pred. No. 2.4e-08; Matches 69: Conservative 43: Mismatches 98: Indels 108: Gaps 11:
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---MFVALLGLGLGQVVCS 63

22 PGAPHEGPLHAPPPPAP----HQPPAASRS-----

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Query Match
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A26868
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                                                                                                   C; Accession: S06286
S; Certa, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.
EMBO J. 6, 4137-4142, 1987
A; Title: A naturally occurring gene encoding the major surface antigen precursor p190 of
A; Reference number: S06286; MUID:88166657
A; Accession: S06286
A; Status: not compared with conceptual translation
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R; Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.;
Mol. Biochem. Parasitol. 27, 291-302, 1988
A; Title: Variation in the precursor to the major merozoite surface antigens of Plasmodiu A; Reference number: A54498; MUID:88142999
A; Accession: A54498
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  malaria parasite (Plasmodium falciparum)
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C;Species: Plasmodium falciparum
C;Date: 28-Oct-1994 *sequence_revision 28-Oct-1994 *text_change 09-Jun-2000
                                                                     C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jun-2000
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A, Molecule type: DNA
A, Residues: 1-1701 < PET>
A, Foresz references: GB:M19143; NID:g160412; PIDN:AAA29653.1; PID:g160413
C, Superfamily: major merozoite surface antiqen
C, Keywords: surface anti-
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C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
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major merozoite surface antigen precursor - malaria parasite (N;Alternate names: 190K protein; polymorphic schizont antigen C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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Pred. No. 19;
4; Mismatches
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Pred. No. 19;
4; Mismatches
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A; Residues: 1-1060 <CER>
S. Superfamily: major merozoite surface antigen
C; Reywords: surface antigen
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A; Molecule type: DNA
A; Residues: 1-1086 < OLA>
A; Cross-references: EMBL:X61930
A; Experimental source: isolate RO-71
C; Genetics:
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1009-QFVKSNSKVITGLTE 1023
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— Best Local Similarity 60.0

— Matches 9; Conservative
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983 QFVKSNSKVITGLTE 997
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Best Local Similarity
Matches 9; Conserv
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C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000
C; Accession: A26868 #sequence_revision 19-Nov-1988 #text_change 09-Jun-2000
R; Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.
J; Mol. Biol. 195, 2373-287, 1987
A; Title: Allelic dimprphism in a surface antigen gene of the malaria parasite Plasmo A; Reference number: A26868; MUID: 88011243
A; Accession: A26868
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Nyliernate names: 195K glycoprotein
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Species: 30-590-1987 ** Resquence_revision 31-Mar-1991 **text_change 09-Jun-2000
C; Accession: A23386; S06361
R; Weber, J.L.; Leininger, W.M.; Lyon, J.A.
Nucleic Acids Res. 14, 3311-3323, 1986
A; Title: Variation in the gene encoding a major merozoite surface antigen of the hum A; Reference number: A23386; MuID:86205236
A; Accession: A23386
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A; Residues: 1-1104 <WEB1>
A; Cross-references: EMBL:X03831
R; Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
A; Title: Merozoite surface protein sequence from the Camp strain of the human malari
A; Reference number: S06361; MUID:88143999
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A Molecule type: DNA
A Molecule stages of different strains have strain-specific surface an C Comment: The merozoite stages of different strains have strain-specific surface an C Comment: P incloparum has three stages: sporozoite, merozoite, and gametocyte. The Superfamily: major merozoite surface antigen
C Meywords: glycoprotein: merozoite; surface 
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F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malaria parasite (Plasmodium falciparum)
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A;Residues: 1-1701 <TANN
C;Superfamily: major merozoite surface antigen
C;Superfamily: major surface antigen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1701/Product: major merozoite surface antigen #status predicted <MAT>
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F;67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-T)
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Length 1701;
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DB 2;
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Pred. No. 31;
4; Mismatches
                                                                                       4; Mismatches
Score 42.5;
Pred. No. 30;
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60.0%;
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60.0%;
57.4%;
60.0%;
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Matches 9, Conserv
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Matches 9; Conserv
Query Match
Best Local Similarity
Matches 9; Conserv
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siderophore/Surfacting synthetase related protein [imported] - Clostridium acetobutyll C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I ; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUD:21359325; PMID:21359325
A; Accession: H97146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE001437; PIDN:AAK79963.1; PID:915024986; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: sainirine herpesvirus 1
A;Note: host Sainiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X64346; NID:g60320; PIDN:CAA45686.1; PID:g60384 R;Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Blesinger, B.; J. Virol. 66, 5047-5058, 1992 A;Tille: Primary structure of the herpesylrus saimiri genome. A;Reference number: A37309; MUID:92333689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, January 1992
A; Description: Primary structure of the herpesvirus saimiri genome.
A; Reference number: A36806
A; Accession: G36812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - saimiriine herpesvirus 1 (strain 11)
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compared with conceptual translation
                                                                       region; immunoglobulin homology
                                                                                                                                                                Length 123;
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A; Note: neither protein nor nucleotide sequence is given
C; Genetics:
A; Gene: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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Pred. No. 30;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                           Pred. No. 3.9;
0; Mismatches
    A;Status: preliminary; not compared with conce
A;Molecule type: mRNA
A;Residues: 1-123 <TAS>
C;Superfamily: immunoglobulin V region; immuno
C;Reywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMA>
                                                                                                                                                                     Score 41;
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Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                   2 YIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                              57 YIKYNEKFKGTTTL 70
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Best Local Similarity
'.hog 7; Conserve
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291 KYIRTNKKFIG 301
                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: G36812
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C; Sgecies: Mus musculus (house mouse)
C; Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change.17-Mar-1999
C; Accession: G48677
R; Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A; Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodic A; Accession: G48677; MUID:94022404
                                                                                                                                                                                 major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C; Accession: A65948
R; Chang, S:P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddigui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A; Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz
A; Reference number: A45948
A; Accession: A45948
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1726 <CHA>
A; Cross-references: GB:M37213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S38635
R;Frommer, G.; Schuh, R.; Jdckle, H.
submitted to the EMBL Data Library, November 1993
A;Description: Localized expression of a novel micropia-like element in the blastoderm A;Reference number: S38635
A;Accession: S38635
A;Accession: S38635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1333 <FRO>
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C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: S38635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: FlyBase:micropia
ross-references: FlyBase:FBgn0014947
, keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.8%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.4%;
60.0%;
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                                                                1026 OFVKSNSKVITGLTE 1040
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127 KYVQARSKMIGSAEL 141
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                                       1 QYIKANSKFI-GITE 14
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hes 9; Conserv
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G48677
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Oy 1 OYIKANSKFIGITE 14 | | | :| :| | ::| | Db • 124 OXITSNATFTGLSE 137 . .

Search completed: October 10, 2002, 15:59:14 Job time : 5.66566 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46; Search time 2.66566 Seconds (without alignments)
540.706 Million cell updates/sec

Title: US-09-787-126-34
Perfect score: 74
Sequence: 1 OYIKANSKFIGITEL 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Scoring table: 283138 seqs, 96089334 residues
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Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	tentoxylysin (EC 3	н	gene 84 protein -	diamine N-acetyltr	hypothetical prote		major merozoite su				O	blastopia polyprot	Ig heavy chain V-D		hypothetical prote		hypothetical prote		oligopeptidase (EC	·	ical pr	heavy	heavy	heavy	heavy chain V		heavy	u	conserved hypothet
	ΙD	BTCLTN	529982	S31029	G86826	T42976	S06286	S16752	A54498	A26868	SAZQGM	A45948	S38635	G48677	H97146	G36812	829980	D85794	G64026	A55485	G86840	S46746	PH1491	PH1516	PH1518	PH1519	F48677	PH1494	PH1488	697978
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	Query Match Length	1315	244	99	180	668	1060	1086	1701	1701	1726	1726	1333	123	447	899	245	79	194	601	109	644	102	119	119	119	123	135	140	189
30	Query	100.0	60.1	59.5	58.1	58.1	57.4	57.4	57.4	57.4	57.4	57.4	56.8	55.4	55.4	55.4	54.7	. 54.1	54.1	. 54.1	54.1	54.1	52.7	52.7	52.7	52.7	52.7	52.7	52.7	52.7
	Score		44.5	44	43	43	42.5	42.5	•	42.5	42.5	42.5	42	41	41	41	40,5	40	40	40	40	40	39	39	39				39	39
	Result No.	-	7	e	7	P	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

A; Accession: B5194 A; Main and a second and a second as a second

A;Molecule type: DNA A;Residues: 743-1315 <FA2> A;Cross-references: GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:g144921 A; Contents: annotation; epitope region
R; Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, Nature 359, 832-835, 1992
A; Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by prote A; Reference number: S27125; MUID: 93063293
A; Contents: annotation

A; Molecule type: protein
A; Residues: 461-475 < MAT>
A; Residues: 461-475 < MAT>
A; Residues: 461-475 < MAT>
B; Demotz. 5.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G. J. Immunol. 142, 394-402, 1989
A; Timunol. 142, 394-402, 1989
A; Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A; Reference number: JSO088; MIDE: 89993918

adenylate kinase (type II restrictio	probable acetyl-Co	type IIS restricti	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	tRNA-pseudouridine	probable hexosyltr	hypothetical prote	hypothetical prote	endo-1,4-beta gluc	cellulase (EC 3.2.	methyl-accepting c	hemagglutinin-neur			•
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KIYMC	B71808	T43043	F64690	C30269	H71875	A64639	F64472	F70361	F71196	T51466	T29127	A86158	T52135	E82395	HNNZ80		ALIGN	-
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213	326	349	423	505	188	188	256	287	381	383	424	501	501	561	572			
52.7	52.7	52.7	52.7	52.7	51.4	. 51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4			- -
36	39	36	36	39	38	38	38	38	38	38	38	38	38	38	38			
	31	32	33	34	35	36	37	30	36	40	41	42	43	44	45			

	RESOLT 1
	BICLIN
	tentoxylysin (EC 3.4.24.68) precursor - Clostridium tetani
	N;Alternate names: tetanus neurotoxin
	C;Species: Clostridium tetani
	C,Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
	C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
	R;Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel
	EMBO J. 5, 2495-2502, 1986
	A; Title: Tetanus toxin: primary structure, expression in E. coli, and homology with
	A; Reference number: A25689; MUID:87053814
	A; Accession: A25689
	A:Molecule type: DNA
	A; Residues: 1-1315 <eis></eis>
	A;Cross-references: GB:X04436; NID:940769; PIDN:CAA28033.1; PID:940770
	R;Fairweather, N.F.; Lyness, V.A.
	Nucleic Acids Res. 14, 7809-7812, 1986
	A; Title: The complete nucleotide sequence of tetanus toxin.
•	A; Reference number: A25757; MUID:87040747
	A;Accession: A25757
	A; Molecule type: DNA
	A; Residues: 1-1315 <fai></fai>
	A; Cross-references: GB: X06214; NID: 940773; PIDN: CAA29564.1; PID: 940//4
	A Experimental source: strain CN3911
	R; Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
	J. Bacteriol. 165, 21-27, 1986
	A, Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C
	A; Reference number: A25194; MUID:86085672
	A; Accession: A25194

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Gaps

6

Length 66 4; Indels

5

DB 2

Weissenbach, J.; El

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diamine N-acetyltransferase (EC 2.3.1.57) [imported] - Lactococcus lactis subsp. lact N;Alternate names: spermidine acetyltransferase C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lacti: A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: G86826
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005176; PID:g12724622; PIDN:AAK05713.1; GSPDB:GN00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 63 - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: G86826
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.;
Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the herpesvirus ateles genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: AF083424; PIDN: AAC95587.1
A; Experimental source: strain 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2
Pred. No. 2.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T42976
R; Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998
A; Description: Primary structure of the herpesvi
A; Reference number: Z22274
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                    Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: yqfF
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.18;
64.38;
                                                                                                                                                                    59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.1
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 QYITSNSTFTGQTE 137
                                                                                                                                                                                                                                                                                     2 YIKANSKFIGITEL 15
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65 IEANDTFIGIVEL 77
                                                                                                                                                                                                                                                                                                                    50 YIKRNGKFVGTWEV
                                                                                                                                                                    Query Match
Best Local Simílarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-180 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T42976
                                                                                  A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT (
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Ayîtle: Superinfection immunity of mycobacteriophage L5: applications for genetic trans
A;Reference number: $30949; MUID:93211283
A;Accession: $31029
                                                                                                                                                                                                                        C;Comment: The source of this protein was an extrachromosomal plasmid.
C;Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C;Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglic C;Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
                  R;de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
Buch, J. Biochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.
R;Reference number: 869348; MUID:95262688
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;2-457/Product: unclaintoproteinase; neurotoxin; transmembrane protein; zinc F;2-457/Product: tentoxylysin light chain (fragment A) #status predicted <TIL>F;461-1315/Product: tentoxylysin heavy chain (fragment B.C) #status experimental <TTH>F;461-864/Domain: channel forming (fragment B) #status predicted <TXB>F;865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC> 333,237/Binding site: zinc (His) #status predicted 234/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: 218946; NID: 915859; PIDN: CAA79460.1; PID: e59702; PID: 9579152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Salmo salar (Atlantic salmon)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999 C;Accession: S31029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNÅ
A;Residues: 1-244 <HOR>
A;Cross-references: EMBL:X70166; NID:g64369; PID:g64370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%; Score 74; DB 1; I
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atlantic salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G. Mol, Microbiol. 7, 407-417, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44.5; DB Pred. No. 1.8; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, October 1992
A;Reference number: S29980
A;Accession: S29982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: tetanus toxin
C; Keywords: hydrolase; metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene 84 protein – Mycobacterium phage L5
C;Species: Mycobacterium phage L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Jest Local Similarity 55.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          class II histocompatibility
                                                                                                                                                                 A; Molecule type: protein A; Residues: 2-31 <DEF>
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Residues: 1-66 < DON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S29982
R; Hordvik, I.
                                                                                                                                            A; Accession: S69348
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Gaps

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Length 180

DB 2;

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Gaps

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Length 899

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October 10, 2002, 12:48:46; Search time 84.9789 Seconds (without alignments) 414.343 Million cell updates/sec
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1 MRRASRDYTKYLRGSEEMGG.....LLDPPQDATYFGAFKVRDID 317
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                      747574 seqs, 111073796 residues
                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

/SIDS1/gcgdata/geneseq/genesegp-embl/AA2001.DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:* /gcgdata/geneseq/geneseqp-embl/AA1989.DAT. /gcgdata/geneseq/geneseqp-embl/AA1990.DAT. /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996 gradata/geneseg/genesegp-embl/AA1998 /SIDS1/gcgdata/geneseq/genesegp-emb1/AA1985. gcgdata/geneseg/genesegp-embl/AA199 /gcgdata/geneseq/geneseqp-embl/AA199 qcqdata/qeneseq/qeneseqp-embl/AA199 dcgdata/genesed/genesedp-emp /SIDS1/gcgdata/geneseq/geneseqp-embl /SIDS1/gcgdata/geneseq/geneseqp-embl /SIDS1/gcgdata/geneseg/ A_Geneseq_032802:* /SIDS1/gcgdata/ /SIDS1/gcgdata/ IDS1 /SIDS1 /SIDS1 /SIDS Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human osteoprotege	NF-kB receptor act	NF-kB receptor act	Amino acid sequenc	Human receptor act	Human receptor act	Human full-length	Osteoclastogenesis	Human osteoprotege	Osteoclastogenesis	Amino acid sequenc
SUMMARIES				1195	957	3293	1417	3738	1426	1993	3018	1194	3017	9654
SOF			a	AAW83	AAW6	AAW68293	AAY84	AAEOE	AAE04	AAE01	AAW83	AAW83	AAW83	AAW59654
			DB	19	19	19	21	22	22	22	19	19	19	19
		Query	Length	317	317	317	317	317	317	317	317	316	316	316
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.5	84.1	84.1	84.1
			Score	1685	1685	1685	1685	1685	1685	1685	1677	1417.5	1417.5	1417.5
		Result	No.	Н	7	m	4	Ω.	9	7	80	6	10	11

. Murine TRANCE. Mu		Amino acid sequenc	Amino acid sequenc	Rat osteoclast dif	NF-kB receptor act	NF-kB receptor act	Murin@ receptor ac	Murine receptor ac	Murine RANKL (rece	Osteoclastogenesis	Human TRANCE. Hom	Amino acid sequenc	A murine OCIF-bind	Amino acid sequenc	Human RANKL. Homo		Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	A murine osteoprot	An osteoprotegerin	An osteoprotegerin	DNA encoding osteo	Mouse OBM protein	An osteoprotegerin	•	Human Apo-2 ligand	~	Human TL2 (TRAIL),	Tumour necrosis fa	Human Apoptosis in	apoptosi	Novel cytokine Apo	
												•	سر	/		Ţ																		
AAY17874	AAY91024	AAY84418	AAY84419	AAB82092	AAW69956	AAW68292	AAE08737	AAE04425	AAE01992	AAW83020	AAY17873	AAB84420	AAW83019	AAB08273	AAB67248	AAU08386	AAY84420	AAY84421	AAB08272	AAY84422	AAY84423	AAY84424	AAY84425	AAY91023	AAY84426	AAY91020	AAY27016	AAY27017	AAW76332	AAW95032	AAW27134	AAW19787	AAW19777	
20	21	21	21	22	13	19	22	22	22	19	20	22	19	21	22	22	21	21	. 21	21	21	21	21	21	21	21	20	20	13	50	18	18	18	
316	316	316	316	318	294	294	294	294	294	246	245	501	244	160	152	170	187	173	160	173	188	. 182	173	139	173	74	281	281	279	279	281	281	281	
84.1	84.1	84.1	84.1	82.9	78.7	. 78.7	78.7	78.7	78.7	8.92	7.97	67.4	65.8	50.6	48.3	46.9	45.8	4516	45.6	45.0	42.8	42.2	41.0	40.5	39.8	18.8	15.0	15.0	14.9	14.9	14.9	14.9	14.9	
1417.5	1417.5	1417.5	1417.5	1396.5	1326.5	1326.5	1326.5	1326.5	1326.5	1294	1293	1136	1109	852	814	190	771	169	168	759	721.5	711.5	691	683	670	317.5	252.5	252.5	251.5	251.5	251.5	251.5	251.5	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	.29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 AAW83195

Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease. Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert. AAW83195 standard; Protein; 317 AA 98US-0052521. 97US-0842842. 97US-0880855. 98WO-US07584. (first entry) Homo sapiens WO9846751-A1 11-FEB-1999 15-APR-1998; 22-OCT-1998. AAW83195;

(AMGE-) AMGEN INC 30-MAR-1998; 16-APR-1997; 23-JUN-1997; Boyle WJ;

WPI; 1998-594578/50. N-PSDB; AAV70285.

WO9828426-A2

us-09-787-126-2.rag

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                                                                                                               The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for
                                                                                                                                                                                                                                                                                                                                                                                    antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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  Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRRASRDYTKYLKGSEEMGGGPGAPHEGPLHAPPPPAPHOPPAASRSMFVALLGLGLGCOV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1685; DB 19; Length 317; 100.0%; Pred. No. 2.6e-156; 1.1ve 0; Mismatches 0; Indels 0;
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                                                                               Claim 19; Fig 4; 47pp; English.
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PDQDATYFGAFKVRDID 317
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                             This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappab (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their
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                                                                                                                                                                                                                                                                                                                New isolated ligand for receptor activator of NP-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
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                                                                                                                                                                                                                        Maraskovsky E;
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                                                                                                       97US-0064671.
96US-0059978.
97US-0813509.
                                                                      97WO-US23775.
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Matches 317; Conservative
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N-PSDB; AAV41378.
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                                                                                                                                                07-MAR-1997;
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                                                                      22-DEC-1997;
                                                                                                           14-OCT-1997;
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PDQDATYFGAFKVRDID 317

301 301

KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV

181

121 QAFQGAVQKELQHIVGSQHIRAEKAMYDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

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                                                                                                                                                                                                                                                                                                                     RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
immune response; inflammatory response; toxic shock; sepsis;
RANKL; RANK ligand; tumour necrosis factor; TNF.
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100.0%; Pred. No. 2.6e-156;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                NF-kB receptor activator RANK ligand (RANKL).
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                                                                     AAW68293 standard; Protein; 317 AA.
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96US-0059978.
97US-0813509.
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N-PSDB; AAV41372.
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Matches 317; Conserv
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23-DEC-1996;
07-MAR-1997;
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The present sequence represents a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The mutine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of open activity in an animal. The method comprises using at least one OPGL depression of the comprises using at least one OPGL definition of the comprises using at least one OPGL definition of the comprises using at least one OPGL definition of the comprises using at least one OPGL definition of the comprises of the comprises of the comprise of the comprises of the comprises of the comprises of the comprise of the comprise of the comprises of the comprise of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis
                                                                                                                                                                                                                                                                                 Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption.
                                                                                                                                                                                                                              Amino acid sequence of a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stalk domain"
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/note= "active ligand moiety"
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/note= "transmembrane region"
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                                                      AAY84417 standard; Protein; 317 AA
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02-OCT-1998;
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Indels

QAEQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPPAHLTINATDIPSGSH 180

61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

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useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
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                                                                                                                                                                                                                   QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
                                                                                                                                                                                                                                                                                                                      YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; receptor activator of nuclear factor kappab ligand; RANKL; NF; tumour necrosis factor; TNF; TNF receptor associated factor; TRAF; immune response; inflammatory response; graft-versus-host reaction; toxic shock; sepsis; acute inflammatory reaction; bone resorption; anti-apoptotic signal; thérapy; immunosuppressant; anti-inflammatory.
                                                                                                              0;. Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New receptor activator of NF-kappaB (RANK) polypeptides, useful for
                                                                                                                                                                                                                                                                     KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
                                                               Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human receptor activator of NF kappaB ligand (RANKL) protein.
                                                                                      0; Indels
                                                          ; Score 1685; DB 21;
; Pred. No. 2.6e-156;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE08738 standard; Protein; 317 AA.
                                                             100.0%;
100.0%;
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97US-0064671.
96US-0772330.
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                                                                                      Matches 317; Conservative
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                                                                         Similarity
                                      317 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001
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                                       Sequence
                                                             Query Match
Best Local
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VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

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241 YVTKTSIKIPSSHTLAKGGSTKIWSGNSEPHFYSINVGGFFKLRSGEEISIEVSNPSLLD

301

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AAE04426 standard; Protein; 317

RESULT 6
AAE04426
ID AAE0

YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD

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The patent discloses novel receptor activator of nuclear factor (NF)-

kappaB (RANK) proteins and their corresponding DNAs. RANK is member

c kappaB (RANK) proteins and their corresponding DNAs. RANK is member

cof the tumour necrosis factor (TNF) receptor superfamily and associates

cof these preceptor associated factor (TRAF) 2 and 3 which are important

in the regulation of immune and inflammatory response. The receptors

cof these receptors. The cytoplasmic domain of RANK is used in developing

assays for inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,

cof these that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,

TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists

cracusoms that result from triggering of RANK, e.g. in treating toxic

sponse that result from triggering of RANK, e.g. in treating toxic

response that result from triggering of RANK, e.g. in treating toxic

creptors and the effects of bone resorption. RANK acts as an anti-

cappitotic signal and rescue the cells that express RANK from apoptosis.

coluble forms of the receptor are used in vivo or in vitro based

contagonists of RANK-mediated NF-kappa B activation, or to inhibit

cransduction of a signal via RANK. RANK compositions are used in the

development of both agonistic and antagonistic antibodies, or as an

confluent therapy for disease characterised by neoplastic cells that

capputor; therapy for disease characterised by neoplastic cells that

capputor; therapy for disease characterised by neoplastic cells that

cappress RANK. Compounds that interfere with RANK/TRAF6 interactions

are useful for modulating the formation of osteoclasts from osteoclast

contagonists of precursors and for modulating osteoclast function and activities. They

are useful for modulating the formation of osteoclasts from prescriptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are used as inhibitors of diseases associated with excess bone resorption and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK-related activity. The present sequence is RANK ligand (RANKL) protein from human.
regulating immune response, in screening for RANK inhibitors, or as an adjunct therapy for disease characterized by neoplastic cells that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HITTELLICATION OF THE TOTAL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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100.0%; Pred. No. 2.6e-156;
ive 0; Mismatches 0;
                                                                                                                                                                                                              Example 15; Column 71-72; 47pp; English
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Best Local Similarity 100.
Matches 317; Conservative
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                                                                                                               express RANK
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                                                                                Human; receptor activator of NF-chi B; RANK; tumour necrosis factor; TNF; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; chromosome 18q22.1; huRANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to receptor activator of NF-chi B (RANK) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for regulating inmune response and in screening for inhibitors of RANK. The present sequence is human RANKL (huRANKL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIFDSCRRIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGGQV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 317;
                                                      Human receptor activator of NF-chi B ligand (huRANKL) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1685; DB 22;
ilarity 100.0%; Pred. No. 2.6e-156;
Conservative 0; Mismatches 0;
                                                                                                                                                                                        162..317
/note="Receptor binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 65-66; 43pp; English.
                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       97US-0077181.
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                            (first entry)
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N-PSDB; AAD08715.
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Best Local Similarity
Matches 317; Conserv
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                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                  US6242213-B1
                                                                                                                                                                                                                                                                                            22-DEC-1997;
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14-OCT-1997;
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AAE04426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
                                                                                                                                                                            Key
Region
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The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor) kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TWF receptor-associated factors (TRAFS). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANKL) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system. Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAS, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target cells for use in gene therapy applications in diagnosing diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; receptod activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; NaNK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO; early onset Paget's disease of bone; EP; cytostatic; chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
for th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    generactivating mutations, associated with e.g. familial expansile osteolysis (FEO) and early onset Paget's disease of bone (EP). The present amino acid sequence is full-length human RANKL (huRANKL) protein. The RANKL gene is located in chromosome 13q14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human full-length RANKL (receptor activator of NF-kappaB ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA encoding a receptor activator of NF-kappaB polypeptide treatment of Paget's disease and Familial Expansile Osteolysis
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llarity 100.0%; Pred. No. 2.6e-156;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                             AAE01993 standard; Protein; 317 AA.
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                                                                                                                    301 PDQDATYFGAFKVRDID 317
                                                                                                                                                          301 PDQDATYFGAFKVRDID 317
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Matches 317; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcifical or parathyroid hormone (PTH).
                                                                                                                                                                                                                                                                                          Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                   QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
                                                                            KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
                                                                                                                                                                                                                                                                           Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM)
      - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein binding to osteoclastogenesis inhibitory factor - usefu
for, e.g. treatment and investigation of disorders of bone and
calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga '
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinosaki M, Kobayashi F,
Takahashi K, Tomoyasu A,
K, Yano K, Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 36; Pages 113-114; 151pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                        (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                            AAW83018 standard; Protein; 317 AA
                                                                                                                                                                                                                                                                                                                                                                                                         97JP-0151434.
                                                                                                                                                                                                                                                                                                                                                                                         97JP-0332241.
97JP-0097808
                                                                                                                                                                                                                                                                                                                                                                          98WO-JP01728
                                                                                                                                                                                                                                                                                                                                                                                                                         97JP-0224803
                                                                                                                                                                              PDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                      301 PDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goto M, Higashio K,
Nakagawa N, Shima N,
Washida N, Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-594563/50.
N-PSDB; AAV69887.
                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                          WO9846644-A1
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12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                          15-APR-1998;
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                                                                                                                                                                                                                                            AAW83018;
                                                                                                                                                                                                                                                                                                             human.
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                                                                                                                                                                                                                     AAW83018
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obm is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                       QAFQGAVQKELQHIVGSQHIRAEKAMYDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                     KVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 YVTKTSIKIPSSHTLMRGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEBISIEVSNPSLLD
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                                                                                                                                                                                                                                                                       Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human osteoprotegerin binding protein from the 32D-F3 ins
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                   Score 1677 DB 19;
Pred. No. 1 6e-155;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                       99.5%;
nilarity 99.7%;
Conservative 0
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97US-0842842.
97US-0880855.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDQDATYFGAFKVRDID 317
                                                                                                                                                                                            components of drugs.
                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 316; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
                                                                                                                                                                                                                              317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paget's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN
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                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                              Query Match
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98WO-JP01728

97JP-0332241

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Unidentified
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                                                                                                                                                                                                                                                                                      The present sequence is human osteoprotegerin (OPG) binding protein.

Host cells transfected with vectors containing nucleic acid molecules
encoding OPG binding protein are used to produce recombinant OPG binding
protein oPG binding protein is used in binding assays to determine
osteoprotegrin (GG) in biological samples; to screen for specific
binding agents (particularly agonists and antagonists, including
intracellular proteins); to raise Ab (useful in immunoassays for
detection of OPG binding protein) and to identify compounds that
modulate binding of OPG binding protein to osteoclast differentiation
and activation receptor (ODAR). The nucleic acid molecule encoding
binding protein can be used to detect OPG binding protein-encoding
c sequences, e.g. screening for related sequences also to produce
transgenic animal models, while complementary sequences are used for
antisense regulation of OPG binding protein expression. Modulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPG binding protein, particularly soluble forms of OPG binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OB osteoclast; bone absorption factor; bone disorder; calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or Ab, aris used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQIM 239
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                                                                                                  Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            optionally in combination with agents that promote bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%; Score 1417.5; DB 19; Lengt liarity 84.3%; Pred. No. 3.8e-130; Conservative 16; Mismatches 31; Indels
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                                                                                                                                                                                                                                       Claim 19; Fig 1; 47pp; English.
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      WPI; 1998-594578/50.
N-PSDB; AAV70284.
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Matches 268;
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      \texttt{RRXFFFXXX} \\ \texttt{SOSSSS} \\ \texttt
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(OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLOLM 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an osteoclastogenesis inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                        Protein binding to osteoclastogenesis inhibitory factor - usefu
for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                    Morinaga
Tsuda E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 84.1%; Score 1417.5; DB 19
Local Similarity 84.3%; Pred. No. 3.8e-130;
les 268; Conservative 16; Mismatches 31;
                                                                                                                                                                                 Kobayashi F,
Tomoyasu A,
                                                                                                                                                                                                                                   Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Pages 106-108; 151pp; Japanese.
                                                                                                                                  SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                 Goto M, Higashio K, Kinosaki M,
Nakagawa N, Shima N, Takahashi K,
Washida N, 'Yamaguchi K, Yano K,
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                                                                             97JP-0224803
                        97JP-0151434
                                                    97JP-0217897
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                                                                                                                                                                                                                                                                                       WPI; 1998-594563/50,
N-PSDB; AAV69886.
                                                                                                                                                                                                                                                                                                                                                                                                         for, e.g. treatment
calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the protein,
15-APR-1997;
09-JUN-1997;
                                                                             21-AUG-1997;
                                                    12-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of 499E9 can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse cell surface antigen, 499E9 protein – used to treat conditions associated with abnormal physiology or development
                                                                                                                                                                                                                                                                                                       Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis; antagonist; autofimmune disorder; rheumatoid arthritis; systemic lupus erythematosus; Hashimoto's autofimmune thyroiditis; acute inflammatory response; antibody; antigen; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19; Length 316;
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larity 84.3%; Pred. No. 3.8e-130;
Conservative 16; Mismatches 31;
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/note= "extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "intracellular domain"
                                                                                                                                                                                                                                              Amino acid sequence of mouse 499E9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                         AAW59654 standard; Protein; 316 AA.
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                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-348452/30.
N-PSDB; AAV41489.
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RESULT 11
AAW59654
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as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents murine TRANCE polypeptides or their cytokines (TRANCE). Human or murine TRANCE polypeptides or their wariants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing Teell activation. These techniques are especially useful for treating immune system related conditions such
                                                                                                                               HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLXANICFRHETSGDLATEYÜDLM 239
                                                                              TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen.
               KOAFOGAVOKELOHIVGSOHIRAEKAMYDGSWLDLAKRSKLEAOPFAHLTINATDIPSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNF like proteins for treating autoimmunity and cancer
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97US-0989479.
98US-0034099.
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N-PSDB; AAX80224.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Murine TRANCE
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                                                                                                                                                                                                                                                                                        RESULT 12
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Sequence

60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119

1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHOPPAASRSMFVALLGLGLGG 59

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of osteoclast in the co-culture of
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02-OCT-1998;
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                                                                                                                                                                                                                   Matches 268;
                                                                                                invention
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                                                                                                                                                                               VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
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                                                                                                                                                                                                                                                                                    VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF; OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH; parathyroid hormone.
                                                                                                                       HKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM
                                                                                                1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGO
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                  20; Length 316;
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                                     .8e-130;
es 31;
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                  84.1%; Score 1417.5;
84.3%; Pred. No. 3.86
                                                            16; Mismatches
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                                       al Similarity
268; Conserv
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mouse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug and a research reagent. The present sequence represents a mouse OCIF binding molecule (OBM) from the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 HKVSLSSWYHDRGWAKISNMTFSNGKLIVNODGFYYLYANICFRHHETSGDLATEYLQLM 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VVCSIALFLYFRAQMOPURISEDSTHCFYRILRLHENAGLØDSTLESEDT--LPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                                                VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 HKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYXLYANICFRHHETSGSVPTDYLQLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 VYVVKTSIKIPSSHNLAKGGSTKNASGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
                                                                                                                                                                                                                                                                                                                                        240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL
                                                                                                                                                                                                            21; Length 316;
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                                                                                                                                                                                                      84.1%; Score 1417.5; DB 21; Lengt
84.3%; Pred. No. 3.8e-130;
.ive 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "extracellular stalk domain"
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158..317
/note= "active ligand moiety"
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98US-0102896
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152..316
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/note=
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Mus musculus
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Best Local
                                             Region
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                                                                                                                                                                                                                                                            OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                      vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
treat, prevent and ameliorate osteoporosis -
                                                                                                                                                    present sequence represents a murine osteoprotegerin ligand (OPGL)
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                                                                                                                                                                                                                                                                                                                                                             Score 1417.5; DB 21; Length 316;
Pred. No. 3.8e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption.
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                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                    84.3%; Pred. No. 3.c. 84.3%; Pred. No. 3.c. ... 16; Mismatches
                                                                                                                             Claim 17; Page 81-82; 110pp; English.
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                                                                                            In vivo down-regulation of
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                                                                                                                                                                                                                                                                                                                                                                                   Matches 268; Conservative
          (MEBI-) M & E BIOTECH AS.
                                 Haaning J;
                                                       WPI; 2000-271444/23.
N-PSDB; AAZ99965.
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                     316 AA;
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                                 Halkier T,
                                                                                                                                                                                                                                                                                                                                        Sequence
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The present sequence represents a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-I. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis
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                                                                                                       /note= "extracellular stalk domain"
158.317
/note= "active ligand molety"
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; Pred. No. 3.8e-130;
16; Mismatches 31; II
                           49..69
/note= "transmembrane region"
70..157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 85-86; 110pp; English.
Location/Qualifiers
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Search completed: October 10, 2002, 16:00:55 Job time : 88.9789 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 10, 2002, 12:48:46; Search time 37.2379 Seconds (without alignments) 329.613 Million cell updates/sec

US-09-787-126-2 1685 1 MRRASRDYIKYLRGSEEMGG......LLDPDQDATYFGAFKVRDID 317 Title: Perfect score:

BLOSUM62 Scoring table: Sequence:

105224 seqs, 38719550 residues rched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		Description	014788 h tumor nec	_	P50591 homo sapien	mus r	P48023 homo sapien	mus	P51749 bos taurus	rattı	homo s		cavia	-	-		_	P79337 macaca fasc		P51742 canis famil		P48094 macaca mula	_		_	P33620 papio sp. (_	papio	ednn	pos		capra	cerv	mus mu	P19101 felis silve
SUMMARIES	-	QΙ	TN11_HUMAN	TN11_MOUSE	TN10_HUMAN	TN10_MOUSE	FAST_HUMAN	FASL_MOUSE	TNF5_BOVIN	FASL_RAT	TNF5_HUMAN	TNF5_FELCA	TNFA_CAVPO	TNF5_CANFA	TNFA_MOUSE	TNFA_RABIT	TNFA_SHEEP	TNFA_MACFA	TN14_HUMAN	TNFA_CANFA	TNFA_HUMAN	TNFA_MACMU	TNFA_PERLE	TNFA_RAT	TNFC_MOUSE	TNFA_PAPSP	TNFA_MARMO		TNFA_HORSE	TNFA_BOVIN .	TNFA_PIG	TNFA_CAPHI	TNFA_CEREL		TNFA FELCA
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	% Query	Match	100.0	84.1	14.9	14.7	11.2	10.9	10.5	10.4	9.4	9.0	8.7	8.6	8.4	8.3	8.1	8.0	8.0	7.9	7.9	•	7.9	7.8	7.7	7.7	7.7	7.7	7.6	7.5	7.5	7.2	7.1	7.0	6.9
		Score	1685	1417.5	251.5	248	189	184.5	176.5	175.5	158.5	152	146	145	141.5	140.5	137	134	134	133	133	133	132.5	131.5	130.5	130	129.5	129	128	126.5	126	122	120	118	117
	Result	No.	-	7	m	₹	'n	9	^	60	6	10	11	12	. 13	14	15	16	17	18	19	20	21	22	23	24	25	. 26	27	28	29	30	31	32	33

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-	TNFC_HUMAN TNFA_MACEU TNFB_MACEU CA11_HUMAN V2A_CMVK TNFB_HUMAN YK22_YEAST V2A_CMVNT YK22_YEAST V2A_CMVNT SK2_CMVNT	ALIGNMENTS	#UMAN STANDARD; PRT; 317 AA. TAN1 HUMAN STANDARD; PRT; 317 AA. 014788; 014723; Q9P203; 16-0CT-2001 (Rel: 40, Created) 16-0CT-2001 (Rel: 40, Last sequence update) 16-0CT-2001 (Rel: 40, Last sequence update)	d superfamily igand) (RANKL (Osteoprotege: F).	Craniata; Catarrhini	l blo Lling .C.,	Med-9568710; Tan HL., Kelley M.J., V., Colombero A., Elliott N., Davy E., Capparelli C , Shalhoub V., Senaldi G.	ytokine .";	;; pubMed=9312132; Arron J., Robinson E., yani E., Bartlett F.S.	f the tumor inal kinase 194(1997).	oral ANCE
	244 1 233 1 1464 1 1464 1 233 1 205 1 205 1 850 1 1694 1		STANDARD; ; Q9P2Q3; ell 40, Creato ell 40, Last	actor ligand in kappa B ligible (Control (Cope) (Co	n). ;; Chordata; ;; Primates;	row, and Peripheral row, and Peripheral 7; pubMed=9367155; Maraskovsky E., Bil Roux E.R., Teepe ithe TNF receptor & the TNF receptor & eall function.";	Pub E., t. R ns	n ligand is a cand and activation (1998).	-317 FROM N.A Les; 12; PubMed=93 J., Arron J. Cayani E., B	gand N-ter 190-2	(ISOFOR ubMed=1 S., Sansible form c
	៰៰៰៷៷៷៷៷៷៷៷៷៷ ៰៰៸៹៙៰៷៷៷៷៷៷៹៹៷	. \$. 281	N STA 14723; Q9 01 (Rel) 01 (Rel)	rosis factor ytokine) iation fa	sapiens (Human) yota; Metazoa; llia; Eutheria; TaxID=9606;	711 Car. 9.7	M N.A node 7661; Timms Ellio Hawk Saros	eri ion 176	73-31 nocytes 160112; Rho J. S., Ca	is a novel li ivates c-Jun Chem. 272:25	FROM ngue; 01752 Kyak kells a sec
	117 116 116 116 116 116 117 117 117 117		LT 1 — HUMAN TN11_HUMAN 014788; 01 16-0CT-200 16-0CT-200 16-0CT-200	Tumor necrosis factor ligan of nuclear factor kappa B l induced cytokine, (FRANCE) differentiation factor) (OD TUFGFII OR RANKL OR FRANCE	Homo sapiens (Hu Eukaryota; Metaz Mammalia; Euther NCBI_TaxID=9606;	SEQUENCE FROM N.A. TISSUE-Bone marrow MEDLINE-98032977; Anderson D.M., Marr Tometsko M.E., Roun Galibert L.; "A homologue of th and dendritic-cell Nature 390:175-179	831.6	Boyle W.J.; "Osteoprotegerin differentiation a Cell 93:165-176(5	INE-THE	TRANCE is that active J. Biol. Cl	SEQUENCE FROM TISSUE-TONGUE MEDLINE-20175 Nagai M. Kyai Cancer cells encoding a se formation.";
	# 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		SUL 11			RR RA R R R R R R R R R R R R R R R R R				R R R R R	

301 PDQDATYFGAFKVRDID 317. |||||||||||||||||||||||301 PDQDATYFGAFKVRDID 317

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                                                                                                                                                                                                                                                                                                                                                                                       Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
Biochem. Biophys. Res. Commun. 269:532-536(2000).

-1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
AUGMENTS ABLILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY
AN IMPORTANT ROLE IN BHANCED BONE-RESORPTION IN HUMORAL
HYPERCALCEMIA OF MALIGNANCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHOPPAASRSMFVALLGLGLGOV 60
                                                                                                                                                           SECRETED (ISOFORM 2).
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE
                                                                                                                                                                                               PRODUCED BY ALTERNATIVE SPLICING:
--- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
WEAK IN SPLEEN, BEIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
PLACENTA, SKELFTAL MUSCLE, STOMACH AND THYROID.
--- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
--- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001263; TNF_5.
InterPro; IPR000478; TNF_family.
InterPro; IPR000478; TNF; 1.
Propon; P0008600; TNF; 1.
SMART; SM00207; TNF: 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; I.
Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN ISOFORM 2).
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766176446348097F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Son send an email to license@isb-sib.ch).
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EMBL; AF053712; AAC3731.1; -.
EMBL; AF013171; AAC51762.1; -.
EMBL; AB037599; BAA90488.1; -.
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317 AA;
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198
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DOMAIN
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Yasuda H., Shima V., Nakagawa N., Yamaguchi K., Kinosaki M., Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.; Osteoclast differentiation factor is a ligand for osteography/Osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKI.";
                                                 035235, 035306;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Receptor activation-
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."; J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
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MEDLINE-98227661; PubMed-9568710;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97460112; PubMed-9312132;
Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
--- AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytokine that regulates osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Thymic lymphoma;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
USD.
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                          316 AA
                                                                                                                                                                                                                                                                                                                                             TNFSF11 OR RANKLIOR TRANCE OR OPGL.
Mus musculus (Mouse).
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Osteoprotegerin ligand is a cyto) differentiation and activation."; cell 93:165-176(1998).
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MEDLINE-98188248; PubMed-9520411;
                                STANDARD;
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                             TN11_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyle W.J.
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                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                          ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH OF WEMBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT PROPOUND GROWTH RETARDATION AT SEVERAL STREET, SITES, INCLUDING THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA, WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN HYPERTROPHIC CHONDROCYTES. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                            SUBCELLUIAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODÈS BUT
NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
TRABECULAR BONE AND LUNG.
DISEASE: DEFICIENCY IN THFSFI1 RESULTS IN FAILURE TO FORM LOBULO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
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34944 MW;
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ProDom; PD008600; TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.3%;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: HOMOTRIMER (POTENTIAL).
-i- SUBCELLUIAR LOCATION: Type II membrane protein (Potential).
-i- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-96111955; PubMed-8777713;
Wiley S.R., Schooley R., Smolak P.J., Din W.S., Huang C.-P.,
Nicholl J.R., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
Goodwin R.G.;
                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
TNFSF10 OR TRAIL OR APO2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Induction of apoptosis by Apo-2 ligand, a new member of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Screaton G.R.;
Jones E.Y. Screaton G.R.;
"Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
MEDLINE-20017054; PubMed=10549288;
Hymowitz S.G., Christinger H.W., Puh G., Ultsch M., O'Connell M.,
Kelley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in a
complex with death receptor 5.";
                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                       Identification and characterization of a new member of the TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                              Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
                                                                                                    281 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   crosis factor cytokine family.";
Biol. Chem. 271:12687-12690(1996).
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Placenta;
MEDLINE-96278649; PubMed-8663110;
                                                                                                                                                                                                                                                                                                                                                                                                                                     family that induces apoptosis.";
Immunity 3:673-682(1995).
                                                                                                                                                                                                                                                              Chordata; Primates;
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Mol. Cell 4:563-571(1999).
                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                Homo sapiens (Human)
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Mammalla; Eutherla;
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                    TN10_HUMAN
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InterPro; IPR003263; TNF 5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_abc.
ProDom; PD00229; TNF: 1.
ProDom; PD0060209; TNF: 1.
ProDom; PD006060; TNF 5; 1.
SWART; SW00207; TNF 1.
PROSITE; PS50049; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; TNF_2; TNF_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 -DSYWDPNDEESMNSPCWQVKW------QLRQLVRKMILRTSEETI-----STVQEKQ 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 ONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAASRSMFVALLGLGLGLGQVVCSVALFFYFRAQMD -- PNRISEDGTHCIYRILRLHENADF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 PSLGQTCVLIVIFTVILQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED---
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLY 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.9%; Score 251.5; DB 1; Length 281; 24.1%; Pred. No. 3.7e-14; tive 61; Mismatches 117; Indels 45.
                                                                                                                                                                                                                                                                                                                                                                                                                     DDAAAF78DAAB2F6D CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor ligand superfamily member apoptosis inducing ligand) (TRAIL protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                     32509 MW;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 QHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDR 191
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16-OCT-2001 (Rel. 40, Last annotation update)
FAS antigen ligand (Apoptosis antigen ligand) (APTL) (CD178 antigen).
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3FEACAB9F0D7D802 CRC64;
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llarity 25.4%; Pred. No. 7.7e-14;
Conservative 52; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 TLESODTKLIPDSCRRIK-------OAFQ----
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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InterPro; IPR003563; TWF_5.

InterPro; IPR003636; TWF_abc.

InterPro; IPR00478; TWF_abc.

Pfam; PF00229; TWF; 1.

Probom; PD0002012; TWF_abc; 1.

Probom; PD008600; TWF_5; 1.

SWART; SW00207; TWF; 1.

PROSITE; PS0049; TWF_1: 1.

PROSITE; PS0049; TWF_1: 1.

Cytokine; Transmembrane; Signal-anchor; App
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33477 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. FAS-ANTIGEN MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT. FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T CELLS, OR BOTH.

- I SUBGUIT: HOMOTRIMER (FROBABLE)

- SUBGCELLOLAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
PRO-RICH.
POLY-PRO.
BY SIMILARITY.
                                               Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
Human Fas ligand: gene structure, chromosomal location and species
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DATABASE: NAME-PROW; NOTE-CD guide CD178 entry;
WWW-ncbi.nlm.nih.gov/prow/guide/3338769674_g.htm".
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Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara
Fusamoto H., Kamada T.;
"Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                  Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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        MEDLINE-95127560; PubMed-7826947;
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InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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ProDom; PD002012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
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HSSP; P06804; 2TNF.
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PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
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211 VYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSS-----YLGAVFNLTSADHLYVNVSE 263
                                                                                                                                                                                                                                                                                    ---PSPPPEKKELRKVAHLTGKSNSRSMP---- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----LPLSHK 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKLRSGEEISIEVSN 295
                                                                                                                                                                                                                                                                                                                                                                   64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENAQFQDTTLESQDTKLIPDSCRRIKQAF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 QGAVQKELQHÇVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peitsch M.J., Tschopp J.J.; "Comparative molecular modelling of the Fas-ligand and other members
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand."; Cell 76:969-976(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94185175; PubMed-7511063;
Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
Suda T., Nagata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FASL_MOUSE STANDARD; PRT; 279 AA.
P41047; Q61217; Q9R1F2;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, East annotation update)
TAS antigne ligand.
TANSF6 OR APTILG1 OR FASL OR GLD.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae;
                                                                                                                                                                                                                                                       182 VSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVY
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
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MEDLINE-95196085; PubMed-7889405;
Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
"The mouse Fas-ligand gene is mutated in gld mice and is part or
                                                                                                                                                                                          98; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING
                                                                                                                                     Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                      184 N-LINKED (GLCNAC. . .) (PC 250 N-LINKED (GLCNAC. . .) (PC 260 N-LINKED (GLCNAC. . .) (PC 31485 MW; ABAGEB358246E9BB CRC64;
                                                                                                                                     11.2%; Score 189; DB 1; 21.7%; Pred. No. 7.6e-09;
                                                                                                                                                                     ; Pred. No. 7.66
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM FASL).
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MEDLINE-95388076; PubMed-7544870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the TNF family.";
Mol. Immunol. 32:761-772(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 LSLVNFEESQTFFGLYKL 281
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INF family gene cluster.
Immunity 1:131-136(1994)
     184
250
260
                                                                                       281 AA;
                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SSLEKOIGH
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CARBOHYD
CARBOHYD
VARSPLIC
VARIANT
VARIANT
                                                                                                SEQUENCE
                                                                                                                            Query Match
                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                CHARACTERIZATION OF VARIANT GLD.
MEDLINE-96091792; PubMed=1495745;
Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
Rousseau M., Bron C., Renno T., French L., Tschopp J.;
"Characterization of the non-functional Fas ligand of gld mice.";
Int. Immunol. 7:1381-1386(1995)
-!-FUNCTION: CYPOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POFENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED LYMPHOPROLIFERATION DISEASE (GLD). AN AUTOSONAL RECESSIVE DISEASE RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION. SIMILARITY: BELONGS TO THE TUNOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              T CELLS, OR BOTH.
SUBUNT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.
ISOFORM FASL IS SOLUBLE.
                                                                                                STRAIN-C3H: TISSUE-Spleen;
MEDLINE-2002164; Pubmed-10552956,
Ayroldi E. D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile E., Migliorati G., Delfino D.V., Riccardi C.;
Cannarile E., Migliorati G., Delfino D.V., Riccardi C.;
Cloning and expression of a short Fas ligand: A new alternatively
spliced product of the mouse Fas ligand gene.";
Blood 94:3456-3467(1999)
               Fenner M.H., Shioda T., Isselbacher K.J.; "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two amino acids."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Signal-anchor; Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-PRO.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease mutation; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO-RICH
                                                                                    SEQUENCE FROM N.A. (ISOFORM FASLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:99255; Tnfsf6.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Priam; Prioc23; TNF; 1.
Prodom; PDOG02012; TNF; 1.
Prodom; PDO08600; TNF_35; 1.
SMART; SM00207; TNF, 1.
PROSITE; PS00021; TNF_1; 1.
PROSITE; PS50040; TNF_1; 1.
Cytokine; Transmembrane; Glycol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U06948; AAA17800.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF119335; AAD52106.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U10984; AAA19778.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB02915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P01375; 4TSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 058995;
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CARBOHYD
CARBOHYD
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN ISOPORM FASLS).
T -> A (IN STRAIN BALB/C).
E -> G (IN STRAIN BALB/C).
F -> L (IN GLD; ABOLISHES BINDING OF FASL TO ITS RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mertens B.E.L.C., Murluki M., Gaidulis L.; "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand and tumor necrosis factor alpha."; Immunogenetics 42:430-431(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------QKELAELREFINQSLKVSSFEKOIANPS----TPSEKKEPRSVAHLTGN- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 ATEYLQLMVIVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 RIKQAFQGAVQKELQHI--VGSQHIRA---EKAMVDGSWLDLAKRSKLEAQPFAHLTINA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 TDIPSGSHKVSLS-SWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 -NQPLNHKVYMRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGAVFNLTSADHLYV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GQVVCSVALFEYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCR 117
                                                                                                                                                                                                                                                                              Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen
GP39).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PAASRSMFVALLGLGL
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                                                                                                                                                                                                                               DB 1; Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                            ; Score 184.5; DB 1;
; Pred. No. 1.8e-08;
45; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AA.
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MEDLINE=96006582; PubMed=7590981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 EVSNPSLLDPDQDATYFGAFKV 313
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258 NISQLSLINFEESKTFFGLYKL 279
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(Rel. 34, Last sequ
(Rel. 39, Last anno
                                                                                                                                                                                 31442 MW;
                                                                                                                                                                                                                                 10.9%;
21.7%;
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                                                                                                                                                                                                                                                                                    70; Conservative
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     248
258
210
210
184
218
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                                                                                                                                                                                 279 AA;
                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                       218
273
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13;
loved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AVKRQGFYXIYTQVTFCSNR-----ETLSQAPFIASLCLKSPSGSERILLRAANTH-- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 RIHENADFQDT--TLESQDTKLIPDSCRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 NLHEDFVFMKTIQRCNKGEGSLSLLNCEEIRSRFEDLVKDIMQ----NKEVKKKEKNFE- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 SWIDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-L 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 IVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKYW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FAS antigen ligand.
THERE OR APTICAL OR FASL.
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TAXID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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"Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor family.";
Cell 75:1169-1178(1993).
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8491FEFB30A787FD CRC64;
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PROSITE; PS50049; TNF 2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
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1larity 24.2%; Pred. No. 7.9e-08;
Conservative 54; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 AA
   modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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InterPro; IPR00478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD008600; TNF_5; 1.
SWART; SM00207; TNF; 1.
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218
240
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DISULFID
CARBOHYD
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EXTRACELLULAR (POTENTIAL).
PRO-PITU
                                                                  -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES, KIDNEY AND LUNG.
-1- INDGCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEURIN-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GSHKVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQ 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 G-----MYQLFHLQKELAELREFTNHSL-RVSSFEKQIANPSTPSETKKPRSV---- 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FVALLGLGL 57
         SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 LMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 HKVYM--RNFKYPGDLVLMEEKKLNYCT-TGQIWAHSSYLGAVFNLTVADHLKVNISQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.

DOMAIN 70 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PRO DOMAIN 100 278 EXTRACELULAR (POTENTIAL).

4 69 PRO-RICH.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                              -! - SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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HOMOTRIMER (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_family.
Probom; PD00209; TNF; I.
Probom; PD002012; TNF_abc; I.
Probom; PD008600; TNF_5; I.
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01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                               Aruffo A.;
"The human T cell antigen gp39, a member of the TNF gene family, is ligand for the CD40 receptor: expression of a soluble form of gp39 with B cell co-simulatory activity.";
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Acutifo A., Farington M., Hollenbaugh D., Li X., Milatovich A., Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M., Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.; The CD40 Ilgand, pp39, is defective in activated T cells from pattents with X-linked hyper-IgM syndrome.";
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Macduff B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
"Recombinant human CD40 ligand stimulates B cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-235.
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MEDLINE-93138085; Pubmed-7678552;
Gauchat J.F.M., Aubry J., Mazzel G.J., Life P., Jomotte T., Elson (
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-93049181; PubMed=1385114;
Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,
Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression by factors controlling IgE production."; FEBS Lett. 315:259-266(1993).
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Eur. J. Immunol. 22:3191-3194(1992).
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M., Terasaki H., Ninomiya R., Shimizu S., Nunoi
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-93076854; PubMed-1280226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exp. Med. 176:1543-1550(1992).
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Protein Sci. 7:1124-1135(1998).
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T-LYMPHOCYTES.

-1-DISEASE: DEFECTS IN THREFS ARE THE CAUSE OF AN X-LINKED IMMUNODEFICIENCY WITH HYPER-IGM (HIGHI); AN IMMUNOGLOBULIN ISOTYPE SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES PRESENT AT AN EARLY AGE (USDALLY WITHIN THE FIRSY TEAR OF LIFE) RECURRENT BACTERIAL MOPPORTUNISTIC INFECTIONS, INCLUDING PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH INTRAVENDUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR, WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
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-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
-!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "CD40 ligand mutations in x-linked immunodeficiency with hyper-IgM."; Nature 361:541-543(1993).
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MEDLINE-9613353; PubMed-8550833;
Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.;
"A single strand conformation polymorphism study of CD40 ligand.
Efficient mutation analysis and carrier detection for X-linked hyper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoni D., Giliani S., Mantuano E., Fasth A., Andersson B., Zegers B.J.M., Disangini G., Reznick I., Levy J., Zan-Bar I., Porat Y., Airo P., Plebani A., Vezzoni P., Notarangelo L.D.;
"Characterization of nine novel mutations in the CD40 ligand gene in partients with X-linked hyper IgM syndrome of various ancestry.";
Am. J. Hum. Genet. 56:898-906(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A., Copeland N.G., Bedell M.A., Edelhoff S., Disteche C.M., Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.; "CD40 ligand gene defects responsible for X-linked hyper-IgM
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Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer
Tata J.-I., Och H.D.;
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STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
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                                                                               Briere F., Padayachee M.,
                                                                                                                                                                                                     Defective expression of T-cell CD40 ligand causes X-linked
VARIANTS HIGM1 ARG-36 AND GLY-140.
MEDLINE-93156839; PubMed-76/9206.
KOTThaeur U., Graf D., Mages H.W., Briere F., Padayachee Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A., de Saint Basile G.;
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MEDLINE-95233438; PubMed-7717401;
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                                                                                                                                                                                                                                                     immunodeficiency with hyper-IgM.";
Nature 361:539-541(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93156840; PubMed-8094231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93174270; PubMed-7679801;
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Hum. Genet. 99:624-627(1997)
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                                                                                                                                                                                                                                                                                                                                                                                VARIANT HIGHL GLU-123
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                                                                                                                                                                           Kroczek
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 NICFRHHETSGDLATEYLQLAVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSEFHFYSIN 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYYLYA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 POIAAHVISEAS----SKTTSVLQW-AEKGYYTMSNNLVTLENGKOLTVKRQGLYYIYA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
Antigen; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure; Antigen; Disease mutation; Polymorphism.

CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 261;
          FTP-"ftp://ftp.expasy.org/databases/cdd0lbase".
DATABASE: NAME-PROW; NOTE-CD guide CD154 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd154.htm".
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/FTId=VAR_007516.
/ -> C (IN HIGM1).
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; Pred. No. 2.7e-06;
53; Mismatches 113;
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/FTId=VAR_007513.
A -> E (IN H1GM1).
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V -> A (IN H1GM1)
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 WWW="http://www.expasy.org/cd401base/";
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ProDom; PD008600; TNF, 1.
SMART; SM00207; TNF; 1.
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Best Local Similarity
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REMBL; AF0/310., ...

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RESP; P29965; TALX.

REMPRO3265; TNF_5.

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-i-SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
-i-SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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"Adjuvant properties of feline CDI54 (CD40 ligand).";
"Adjuvant properties of feline CDI54 (CD40 ligand).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF COSTIMUTUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
INVOLVED IN IMMUNOGLOBULIN CLASS. SMITCHING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (F
349FA0391FB7B932 CRC64;
277 VGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                            :|| |:|: |::|::|| : || |::|| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-1001 (Rel. 40, Last annotation update)
TNFSF5 OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                               260 AA.
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217 PO
239 N
28727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 239
260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9685
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                                                                                                                                                                                                                                                                                                                                                                                                                           TNF5_FELCA
097605;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor-alpha.";
Am. J. Physiol. 273:L524-L530(1997).
Am. J. Physiol. 273:L524-L530(1997).
-I- FUNCTION: TWF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN THORN CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYRGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-97462215; PubMed-9316485; White A.M., Wostwick J., Watson M.L.; White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.; alrway inflammation induced by recombinant guinea pig tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE II MEMBRANE PROFEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY). PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
-----MOKGDQDPRVAAHVISEAS-----SSTASVLQW-APKGYYTISSNLVTLENGKQ 159
                                           PROTEOLYTIC PROCESSING (BY SIMILARITY).
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
                          206 LIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIP--SSHTLMKGGSTKY
                                                                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                264 WSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                ol-CCT-1996 (Rel. 34, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Tumor necrosis factor precursor (TNR-alpha) (Cachectin).
TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                Yuan H.T., Kelly F.J., Bingle C.D.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNETROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SNART; SM00207; TNF; 1.
PROSITE; PS00251; TNF, 1.
PROSITE; PS0049; TNF_1; 1.
                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last seq 30-MAY-2000 (Rel. 39, Last annotation)
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-HARTLEY; TISSUE-Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U39839; AAB06492.1; -. EMBL; U77036; AAB19210.1; -.
                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-DUNKIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALNUTRITION.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10141;
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                                                                                                                                                                               TNFA_CAVPO
                                                                                                                                                                  TNFA_CAVPO
112
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                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Signal-anchor.
79 BY SIMILARITY.
34 TUNOR NECROSIS FACTOR.
56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                          134 IVGSQHIRAEKAMVDGSWLDLAKRSKLEA-----QPFAHLTINATDIPSGSHKVSLSS 186
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFSF5 ÓR CD40LG OR CD40L.
Canis familiaris (Dog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                  187 WYHDRGWAKISN-MTFSNGKLIVNQDGFYYLYANICPRHHETSGDLATEYLQLMVYVTKT
                                                                                                                                                                                                                                                                                                                                                                             SIKIPSSHTLM-------KGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEV
                                                                                                                                      ξi...
                                                                                                                                        Length 234;
                                                                                                                                                                             75; Indels
                                                                             BY SIMILARITY.
7272C940393E7E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
CYLOKine; Transmembrane; Glycoprotein; Signal-anchor.
DOMAIN 1 2.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                      ; Score 146; DB 1;
; Pred. No. 2.7e-05;
30; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
                                                                             178 B
25793 MW;
                                                                                                                                          8.78; 25.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF086711; AAD04375.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 NLPQYLDFADSGQIYFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 SNPSLLD-PDQDATYFG 309
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
    Cytokine; Cytotoxin;
PROPEP 1
                                        80 2
36..
147 1
234 AA;
                                                                                                                                                             Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
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16-OCT-2001
CD40 ligand.
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                                                             TRANSMEM
DISULFID
SEQUENCE
                                                                                                                                          Query Match
                                            CHAIN
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                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                 246
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                                                                                                                                                                                                                                                                                                           170 VYAQVTFCSNRAASSQAP-----FVASLCLHSPSGTERVLLRAASSR---GSSKPCGQ 219
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                    42 PAASRSMFVALLGLGL-GQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQ 100
                                                                                                                                                                                                                               101 DTTLESQ--DTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRS 158
                                                                                                                                                                                                                                                             67 KTLQKCNKGEGSLSLLNCEEIKSQFEAF----LKEIMLNNEWKKEENIA------MQKG 115
                                                                                                                                       Gaps
                                                                                                                                                                                       coli of the cDNA for murine
                                                                                                                                                                                                                                                                                                                                                      LYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTKYWSGNSE-FHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE-88224564; PubMed-2836146; Shiral T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.; Cloning and expression in Escherichia coli of the gene for mouse
                                                                                                                                                                                                                                                                                           159 KLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISN--MTFSNGK-LIVNQDGFYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of a common nucleotide sequence in the 3'-untranslated region of mRNA molecules specifying inflammatory
                                                         N-LINKED (GLCNAC. . .) (POTENTIAL). 604F69A19E98EB70 CRC64;
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                                                                                                      Length 260;
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Pennica D., Hayflick J.S., Bringman T.S., Palladino M.A.,
Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-86149365; PubMed-2419912;
Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P06804; 062326;
01-JAN-1988 (Rel. 06, Created)
01-MAY-1989 (Rel. 10, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
               (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 220 QSIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFGLLKL 260
                                                                                                                                                                                                                                                                                                                                                                                                                 273 YSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                       Pred. No. 3.7e-05;
58; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
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                                                                                                         8.6%; Score 145; DB 1;
33.1%; Pred. No. 3.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AA
                                            POTENTIAL.
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                                                                          28688 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor necrosis factor.";
DNA 7:193-201(1988).
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                            260
 46
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SEQUENCE FROM N.A.
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TNFA_MOUSE
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MEDLINE-88067722; PubMed-3684584; MEDLINE-88067722; PubMed-3684584; Semon D., Kawashina E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.; Semon D., Kawashina E., Jongeneel C.V., Shakhov A.N., nedospasov S.A.; Nucleotide sequence of the murine TMF locus, including the TMF-alpha (tumor necrosis factor) and TMF-beta (lymphotoxin) genes."; Nucleic Acids Rès. 15:9083-9084(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.
MEDLINE-99190564; Pubmed-10089307;
Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;
The structure of mouse tumour-necrosis factor at 1.4 A resolution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T., Takekawa K., Ogihara T.; "Identification of a new susceptibility locus for insulin-dependent diabetes mellitus by ancestral haplotype congenic mapping."; J. Clin. Invest. 96:1936-1942(1995).
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              Tizard R., van Heuverswyn H., van Vliet A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in a larger, inactive form of secreted protein."; J. Biol. Chem. 264:16256-16260(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kriegler M., Perez X., Defay K., Albert I., Lu S.D.;
"A novel form of TNF/cachectin is a cell surface cytotoxic transmembrane protein: ramifications for the complex physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherry B., Juc D.-M., Zentella A., Cerami A.;
"Characterization of high molecular weight glycosylated forms of
murine tumor necrosis factor.";
Blochem. Blophys. Res. Commun. 173:1072-1078(1990).
Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliv
Ruysschaert M.-R., Fiers W.;
"Molecular cloning of mouse tumour necrosis factor cDNA and its
eukaryotic expression.";
                                                                                                                                                      Shakhov A.N., Nedospasov S.A.; "Molecular cloning of genes coding for tumor necrosis factor. Complete nucleotide sequence of the genome copy of TNF-alpha in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION OF MEMBRANE-BOUND FORM
                                                                                  Nucleic Acids Res. 13:4417-4429(1985)
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CTS, AND NOD;
MEDLINE-96013654; PubMed-7560085;
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                                                                                                                                     MEDLINE-87298639; PubMed-3040015;
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Cell 53:45-53(1988).
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                                                                                                                     SEQUENCE FROM N.A.
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necrosis factor precursor (TNF:alpha) (Cachectin).

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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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PROSITE; PS50049; TNF_2; 1.
Sytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
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SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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.ive 28; Mismatches 57; Indels
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16DD2A9676D68C5D CRC64;
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InterPro; IPR000478; TNF_family.
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ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
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AAA40459.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITO H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T., Kayashi H., Kato M., Seko M.;

"Molecular cloning and expression in Escherichia coli of the CDNA coding for rabbit tumor necrosis factor.";

"MOIST TAP 156 (1986).

"HITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLKIS OF CERFAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL PROLIFERRATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
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SUBURILUIAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
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-!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
                                                                                                                                                                                                                                                                                                                                               genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDILINE-66219712; PubMed-3519138; Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W., Wallace R.B.;
                                                                Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00229; TNF; 1.
PRIME; PR01229; TNF; 1.
SMART; SM002012; TNF; 1.
SMART; SM00207; TNF; 1.
PROSTIE; PS00231; TNF, 1.
PROSTIE; PS0021; TNF, 2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
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                                                                                                                                                                                                                                                                                                                                           "Structural analysis of the rabbit TNF locus, containing the
                                                                                                                                                                                                                                                                       Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eui
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
INF OR TNFA.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                          MEDLINE-91065534; PubMed-2249779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-86219711; Pubmed=3519137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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PIR; A25454; A25454.
PIR; JS0727; JS0727.
HSSP; P06804; 2INF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sene 95:215-221(1990).
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                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID-9986;
                                                                                                                                                                                                                                                                                                                  Medospasov S.A.
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-!- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
                                                                                                                                                                                                                NRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVG 136
                                                                                                                                                                                                                                                                         137 SQHIRAEKAMYDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKI 196
                                                                                                                                                                                                                                                                                                       ----ASRALSD------KPLAHVVAN----PQVEGQL---QWLSQRANALL 116
                                                                                                                                                                                                                                                                                                                                     SN-MTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTL 255
                                                                                                                                                                                                                                                                                                                                                     256 MKG-------GSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD-PD 302
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                  65
                                                                                                                                                    ---QMDP 76
                                                                                                                                                                                14 EGPL----PKKAGGPOGSKRCLCLSLFSFLLVAGATTLFC----LLHFRVIGPQEEEQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with cloning by inverse PCR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92155784; PubMed-1786996;
Andrews A.E., Nash A.D., Barcham G.J., Brandon M.R.;
"Molecular cloning, expression and characterization of ovine TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91067496; PubMed-2251151;
Young A.J., Hay J.B., Chan J.Y.C.:
"Primary structure of ovine tumor necrosis factor alpha cDNA.";
Nucleic Acids Res. 18:6723-6723(1990).
                                                                                                                       Indels 113;
                                                                                         DB 1; Length 235;
                                                                                                                                                     EGPLHAPPPPAPHQPPAASR - - - SMFVALLGLGLGQVVCSVALFFYFRA - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tumor necrosis factor precursor (TNF-alpha) (Cachectin).
                                            MISSING (IN REF. 3).
610177D0BD2EF871 CRC64;
                                                                                        8.3%; Score 140.5; DB 1;
21.5%; Pred. No. 7.9e-05;
ive 36; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AA.
                                                                                                                                                                                                                                            NNL----HLV-----NPVAQMVTLRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JEDLINE-92112044; PubMed-1765267;
                                               63 1
25816 MW;
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                                                                                                                       66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sardan D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sene 109:203-210(1991)
   235
56
179
                                                           235 AA;
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CONFLICT
SEQUENCE
                 TRANSMEM
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   CHAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL ANCHOR (TYPE-II MEMBRANE PROFEIN).
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
MISSING (IN REF. 1).
4BCFBCCAB7956B88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
                                                                    CONDITIONS.
SUBGNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 IVGSQHIRAEKAMVDGSW---LDLAKRSKLEA---QPFAHLTINATDIPSGSHKVSLSSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- ETSGDL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211
                                                                                                                                                  PROTECLYTIC PROCESSING.
-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PPROGEN CAUSING FEVER BY DIRECT ACTION OR STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGERISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                 BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71; Indels
                                                                                                                                 -! - PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 YHDRGWAKISNMTFSNG-----KLIVNQDGFYYLYANICFRHH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.1%; Score 137; DB 1; 26.1%; Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 M
25536 MW;
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SMART; SM00207; TNF; 1.
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PIR; S20661; S20661.
PIR; JH0529; JH0529.
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PROPEP 1 7
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Best Local Similarity
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Search completed: October 10, 2002, 16:04:50 Job time: 41.2379 secs

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    protein search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_unclassified:* sp_vertebrate:* sp_bacteriap:* sp_archeap:* sp_organelle:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_rvirus:* sp_rodent:* sp_virus:* sp_plant:* sp_human:* sp_phage: * SPTREMBL_19:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q96q17 homo sapien	Q9r1y0 mus musculu	Q9ese2 rattus norv	Q9jjk9 mus musculu	Q9jjk8 mus musculu	. Q91zi9 rattus norv	Q9ddz5 brachydanio	Q90wt9 gallus gall	Q9bea8 sus scrofa	Q95m04 sus scrofa	Q95n10 sus scrofa	O9my16 macaca neme	09bdm5 macaca mula	Q9bdn1 cercocebus	Q9bdn3 callithrix	Q9bdm3 aotus trivi
SUMMARIES	ID	096017	Q9R1Y0	Q9ESE2	Q9JJK9	9371К8	Q91219	Q9DDZ5	090WT9	Q9BEA8	Q95M04	Q95N10	O9MYL6	Q9BDM5	Q9BDN1	Q9BDN3	Ф9врм3
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خد	Query Match	84.4	83.6	82.9	75.4	53.9	15:5	14.3	12.8	11.9	11.9	11.8	11.0	10.9	10.8	10.1	9.9
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DIKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAH 167

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	NMENTS 270 AA. 270 AA. (quence update) notation update) notation update) notation update) notation update) notation update) sats; Vertebrata; rhini: Hominidae rhini: Hominidae 1422; DB 4; Le No. 1.1e-121; matches 0; I
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PRELIMINARY;
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Matches 262; Conserv
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01-OCT-2000 (
01-OCT-2000 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A., Ueda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPAASRSWFLALLGLGLGCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ
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                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 313;
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ProDom; PD008600; TNF_5; 1.
SMART; SM02007; TNF; 1.
SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;
                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0STECCLAST DIFFERENTIATION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.6%; Score 1409; DB 11;
84.3%; Pred. No. 2.1e-120;
ive 16; Mismatches 28;
                                                                                                                                                                              313 AA
                  AB022039; BAA36970.1; -. AB022036; BAA36970.1; JOINED. AB022037; BAA36970.1; JOINED. AB022038; BAA36970.1; JOINED. P50591; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99214075; PubMed-10196481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR003263; TNF_5.
Interpro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4SSP; P50591; 1D0G.
4GD; MGI:1100089; Infsf11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterizat differentiation factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.3
Matches 268; Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 230:121-127(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                           Q9R1Y0
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Q9R1Y0
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RESULT 3 Q9ESE2

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180 HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoni
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE-20540945; PubMed-11092398;
Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wysocki
Zheng M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50049; TNF_2; 1.
SEQUENCE 318 Aa; 35370 MW; 4B87A4D706AD098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning, sequence and functional characterization of homologue of receptor activator of NF-kB ligand."; J. Bomen Miner. Res. 15:2178-2186(2000).

BERBL, AF1871319; AAG17031.1; -. HSSP; P50591; 1DGG.
InterPro; IPR003263; TNF_5.
InterPro; IPR003263; TNF_5.
ProDom; PD008600; TNF_5; 1.
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPPOR ACTIVATOR OF NF-KB LIGAND 2.
                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
10-BEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KB LIGAND.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
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Pred. No. 3e-119;
9; Mismatches 3
318 AA.
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                                                                                    Created)
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SEQUENCE FROM N.A.
MEDLINE-21150053; Pubmed-11250921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
PRT;
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ive 19;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00207; TNF; 1.
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IPR000478; INF_family
InterPro;
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                                                                                     Query Match
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Q91ZI9
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MEDLINE-21150053; PubMed-11250921;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of Three Isoforms of the Receptor Activator of Nuclear Factor-kappab Ligand and Their Differential Expression in Bone and
                                                                                                                                                                                                                                                                                                                                 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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                                                                                                                                                                                                                                                                                                  30; Gaps
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             "Determination of Three Isoforms of the Receptor Activator of Nuclo
Factor-kappaB Ligand and Their Differential Expression in Bone and
                                                                                                                                                                                                                                            1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
            of the Receptor Activator of
                                                                                                                                                                                                 Length 287;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                           8B2CE8E4C7B534CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                              75.4%; Score 1271; DB 11;
77.3%; Pred. No. 7.4e-108;
iive 16; Mismatches 26;
  Utsuyama M., Hirokawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinology 142:1419-1426(2001).
EMBL; AB032772; BAA97258.1; -.
HSSP; PS0591; IDGG.
MGI:1100089; Tnfsf11.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_5.
                                            Endocrinology 142:1419-1426(2001)
                                                                          MGD; MGI:1100089; Tnfsf11.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pf00229; TNF; 1.
                                                      EMBL; AB032771; BAA97257.1; -. HSSP; P50591; 1D0G.
                                                                                                                                                                                                                                                      PROSITE; PS50049; TNF_2; 1.
SEQUENCE 287 AA; 32234 MW;
                                                                                                                                ProDom; PD002012; TNF_abc; 1. ProDom; PD008600; TNF_5; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-007-2000 (TrEMBLrel. 15, 01-007-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, RECEPTOR ACTIVATOR OF NF-KB
                                                                                                                                                                                                Ouery Match
Best Local Similarity 77.3%
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 PDQDATYFGAFKVQDID 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
   Kasai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                    hymus.
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EMBL; AF425669; AAL23963.1; --
                                                                                                                                                                                                                                                                                                                                                                           61 SHKVTLSSWEIDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHETSGSVPTDYLQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 IKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSG 178
                                                                                                                                                                                                                                                                                                                                                     179 SHKVSLSSWYHDRGWAKISNWTFSNCKLIVNQDGFYYDYANICFRHHETSGDLATEYLQL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                              MYYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                         ŭL.
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                                                                                                                                                              Length 199;
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Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF-abc; 1.
ProDom; PD008600; TNF-5; 1.
SMART; SM02007; TNF-2; 1.
PROSITE; PS5049; TNF-2; 1.
SEQUENCE 199 AA; 22150 MW; 401C13EB5EBCE166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 AA; 5876 MW; 8A71E32F2B6A9410 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 8.3e-17;
5; Mismatches 0;
                                                                                                                                                                   DB 11;
                                                                                                                                                                 ; Score 909; DB 11;
; Pred. No. 4.8e-75;
11; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
TRAIL-LIKE PROTEIN.
TRAIL-LIKE PROTEIN.
Brachydanio rerio (Zebrafish) (Zebra danio).
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                                                                                                                                                                 53.9%;
85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 LDPDQDATYFGAFKVQDID 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 LDPDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.5%;
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                                                                                                                                                                                                Best Local Similarity 85.44
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 90.6
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10116;
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140 I-RAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIP-
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InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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PD002012; TNF_abc; 1.
PD008600; TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
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                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00207; TNF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                 307 YFGAFKV 313
                                                                                                                                                                                                                       11111:
279 YFGAFRL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9823;
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                                                                                                         161
                                                                                                                                                                                                                                                                                    RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEELRCLQLINQQQEGSNLEEL-----ISNQSCLKLANTIKAYVATVTENVISRSV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 S------GSHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 RHHETS-GDLATEYLQLMVYV-TKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAK-RSKLEAQPFAHLTINATDIP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SPPQSDMHQPQFDLHQSCRHPVHTWANKSFGAHLXNWTLTNGRLRVPQDGRYXLYSQVYF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.;
"TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bobe J., Goetz F.W.;
"Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary.";
Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
EMBL: AF250041; AAG47640.1;
HSSP; P50591; 100G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.8%; Score 216.5; DB 13; Length
Best Local Similarity 24.7%; Pred. No. 1.3e-11;
Matches 61; Conservative 57; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                    ; Score 240.5; DB 13; Length; Pred. No. 5.4e-14; 50; Mismatches 83; Indels
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Submiriated (OCT-2001) to the EMBL/GenBank/DDBJ databaşes.
EMBL; AY057941; AAL23702.1; -.
SEQUENCE 287 Aa; 32092 MW; DB06E1C95087B108 CRC64;
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                                                                                                                                                                                                                                                                                                                                     214 AA; 24093 MW; 98C002474FF691AA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque
01-DEC-2001 (TREMBLrel. 19, Last annot
TNF-RELATED APOPTOSIS INDUCING LIGAND
Gallus gallus (Chicken)
                                                                                                                                                                                      ETIN, 208-GENE-010801-1; tnfsf101.
InterPro; IPR003263; TNF_5.
InterPro; IPR003663; TNF_abc.
InterPro; IPR004478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD00802012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF, 1.
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                                                                                                                                                                                                                                                                                                                                                                  14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      PROSITE; PS50049; TNF_SEQUENCE 214 AA; 24
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                  SEQUENCE FROM N.A.
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                                                  NCBI_TaxID=7955;
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"Cloning and potential utility of porcine Fas ligand: overexpression
in porcine cells protects them from attack by human cytolytic cells.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB021297; BAB400919.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ELRKVAHLTGK 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----17ELRESASORHT----- 124
                                                                                                                                                      EDSTIHSHLONITYRDGRLRVNQAGKYIVYSQIYFRYSRDGAGARVSVPQLVQCINWKTS 220
                                                                                                                                                                                                                                 IKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDAT 306
                                                                                                                                                                                                                                                               221 YSQPI--LILKGVGTKCWAPEAEYGLHALYQGGLFELKAGDELFYSVSSIAIDYSDAAAS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FVA 51
SGSHKVSLSSW 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
Molecular cloning, characterization, and expression of porcine Fas
ligand (CD95 ligand).";
J. Interferon Cytokine Res. 21:305-312(2001).
                                    YHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVT-KTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 122;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS-LIGAND (FAS LIGAND).
Sus scrofa (Pig).
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3.9e-10;
ches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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13;

Gaps

Indels 118; Length 282;

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54 GLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GIGLG------MFQLFHLQKE------124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 DSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--IN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 -NQPLSHKVY-TRNS-RYPQDLVLMEGKMMNKCTTGQMMARSS------YLGAVFNLTS 254
                                                                                                                                                        Zhu N., Young Y.;
"Molecular cloning and characterization of porcine Fas ligand cDNA.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY033634; AAX56449.1;
                                                                                                                                                                                                                                                                                                                                                                                          22 PGAPHEGPLHAPPPPAPHQPP-AASRSM-----FVALL 53
                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca nemestrina (Pig-tailed macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ATDIPSGSHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 ATEYLQIMVYVTKTSIKIPSSHTIMKGGSTKY-----WSGNSEFHFYSINVGGFFKLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-M.fascicularis; STRAIN-CYNOMOLGUS MONKEY;
Kirii Y., Inoue T., Yoshino K.;
"Cynomolgus monkey Eas ligand mRNA, complete cds.";
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-M.nemestrina; STRAIN-PIG-TAILED MONKEY;
Kiril Y., Inoue T., Yoshino K.;
"Pig-tailed monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               56449.1; -. 31752 MW; F391212406AE1E7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                  11.8%; Score 1993, DB 6; 22.9%; Pred. No. 4,9e-10;
                                                                                                                                                                                                                                                                                                                                       43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
SPECIES-M.mulatta; STRAIN-RHESUS MONKEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 ADHLYVNVSELSLVNFEESKTFFGLYKL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PT-FASL OR CM-FASL OR RM-FASL.
                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9545, 9541, 9544;
                                                                                                                                                                                                                                                                                                                                                   75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecinae; Macaca
                                         Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                                                                                                                                                                                                                          282 AA;
                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                  SEQUENCE FROM N.A.
                   Sus scrofa (Pig).
                                                                                        NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAS LIGAND
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
Q9MYL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
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                                                                                                                 230 DLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKL 283
                                                                                                                                            205 ---NQPLSHKVY-TRNS-RYPQDLVLMEGKMMNYCTTGQMWARSS-----YLGAVFNL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 LLGLGLGQVVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 IPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT-- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ESSLEKQIGHPNLPSEKK------ELRKVAHLTGK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 DLATEYLQLMYYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEFHFYSINVGGFFKL 283
                      170 INATDIPSGSHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHFTSG 229
                                              |: || |------EMEDIYGIALVSGVKYMKGSLVINDTGLYFVYSKVYFRGOYCN- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVGLGLG------MFQLFHLQKE-------LTELRESASQRHT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 INATDIPSGSHKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BREED LANDRACE X LARGE YORKSHIRE WHITE (LW); TISSUE-LIVER; Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.; "Genomic Sequence Analysis of Pig Fas-Ligand Gene."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB069764; BAB64291.1; -- SEQUENCE 282 AA; 31722 MW; E54774EBF455127B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Sulna; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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23.0%; Pred. No. 3.9e-10;
tive 42; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 AA
                                                                                                                                                                                                                                                                                                                                                                              282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 PGAPHEGPLHAPPPAPHQPPAA---SRSM-----
                                                                                                                                                                                                                                  284 RSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, (TrEMBLrel. 19, 1
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                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095N10;
01-DEC-2001
01-DEC-2001
01-DEC-2001
FAS LIGAND.
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01-DEC-2001
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095N10
ID 095N1
AC 095N1
DT 01-DE
DT 01-DE
DE FAS L
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Q95M04
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268 FEESQTFFGLYKL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 PDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBBDN1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 VSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQAF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 QGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 VTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------- MFVALLGLGLGQVVCS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 186; DB 6; Length 280;
22.1%; Pred. No. 7.4e-09;
Live 44; Mismatches 103; Indels 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nonhuman primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiril Y., Inoue T., Yoshino K.;
"Rheaus monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035140; BAA90296.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29043; 1NF_£; 1:
280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FAS ANTIGEN CD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003263; TNF_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                               | InterPro; | IPR003263; | TNE 5. | | |
| InterPro; | IPR0036363; | TNE 5. |
| InterPro; | IPR000478; | TNE abc. |
| InterPro; | IPR000478; | TNE family. |
| Pfam; | PF00229; | TNF; | 1. |
| PRINTS; | PR01234; | TNECROSISFCT. |
| PRODOM; | PD002012; | TNE abc; | 1. |
| PRODOM; | P0008060; | TNE abc; | 1. |
| PROSITE; | PS00251; | TNE abc; | 1. |
| PROSITE; | PS50049; | TNE abc; | 1. |
| PROSITE; | PS50049; | TNE abc; | 1. |
| PROSITE; | PS50049; | TNE abc; | 1. |
| PROSITE; | PS50049; | TNE abc; | 1. |
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| PROSITE; | PS50049; | TNE abc; | 1. |
| PROSITE; | PS50049; | PS50049; | TNE abc; | 1. |
| PROSITE; | PS50049; | P
                                                                                                                       EMBL; AB035139; BAA90294.1; -. EMBL; AB035139; BAA90295.1; -. HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 22.18 tes 69; Conservative
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269 EESQTFFGLYKL 280
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124 --SSLEKQIGH-----158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 PPPPPPPPL-+PPPPPPPPPPPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLG---- 99
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
Cercopithecinae, Cercocebus.
NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 PGAPHEGPLHAPPPPAPHQPP-----AASRS------MFVALLGLGLGQVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ---MFQLFHLQ-------KELAELRESTSOKHTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonhuman primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99;
                                                                                                                                                                                                                                                                                                                                                                         5; DB 6; Length 280;
[e-08;
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InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
InterPro; IPR00478; TNF_1.
InterPro; IPR00229; TNF; 1.
InterPro; PR01234; TNFCACSISFCT.
IPR0Dan; PD002012; TNF_abc; 1.
IPR0Dan; PD008000; TNF_5; 1.
IPR0SITE; PS0027; TNF; 1.
IPR0SITE; PS00249; TNF_1: 1.
IPR0SITE; PS0049; TNF_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.9%; occ. 16-08;
Best Local Similarity 22.4%; Pred. No. 4e-08;
Matches 70; Conservative 44; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                          KVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
                                                                                                                                                                                                                                               SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIKQA 122
                                                                                                                                                                                                                                                                                                                     123 FQGAVQKELQHIVGSQHIRAEKAMYDGSWLDLAKRSKLEAQPFAHLT--INATDIPSGSH 180
                                                                                                                                                                                                                                                                                                                                                     ----PSPPPEKKEQRKVAHLTGKPNSRSMP---- 158
                                                                                                                                                                                                                                                                                                                                                                                                                          ----LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFR-----GOSCTN-LPLSH 208
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                                                                                                                                                                          22 PGAPHEGPLHAPPPPAPHQPP-----AASRS------MFVALLGLGLGQVVC 62
                                                                                                                                                                                                46 PPPPPPPL--PPPPPPPLPPLFPLKKRGNHSTGLCLLVMFFMVLVALVGLGLG----99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-238(2001).

EMBL; AF344844; AAK37603.1; IMSSP; PS9965; IMLY.

InterPro; IPR003563; TNF. 5.

InterPro; IPR00478; TNF_family.

Prop. Proc. 20029; TNF; 1.
                                                                                                                                                                                                                                                                                  ------KELAELRESTSOKHTA------
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                                                                                                       Length 280;
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Weiss W.R., Ansari A.A.;
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                                                                     729EA60067B7D398 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                         DB 6;
                                                                                                                                           44; Mismatches 100;
                                                                                                                       Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA
                                                                                                       10.8%; Score 182.5; 22.4%; Pred. No. 1.5
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Prodom; PD008600; TNF_5; 1.
SMART; SM0207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS550049; TNF_2; 1.
SEQUENCE 280 AA; 31407 MW;
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PROSITE; PSO0251; TNR_1; 1.
PROSITE; PS50049; TNR_1; 1.
SEQUENCE 261 AA.
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                                                                                                                                             70; Conservative
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Best Local Similarity
Matches 71; Conserv
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Matches 70; Conserv
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                                                                      SEQUENCE
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Q9BDN3
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Search completed: October 10, 2002, 16:03:00 Job time : 107.166 secs

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Sequence Sequence Sequence Sequence Sequence

US-08-249-189-12

ALIGNMENTS

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US-09-290-640-25
US-09-479-524-3
US-08-339-214-30
US-08-339-214-30
US-08-339-214-24
US-08-339-214-24
US-08-339-214-24
US-08-339-214-26
US-08-339-214-16
US-08-339-214-26
US-08-184-422-8
US-08-184-422-8
US-08-184-6055-4
US-08-431-055-4

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

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COMPUTER RELABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08996139
Sequence 13, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MACH 1997
PRIOR APPLICATION NUMBER: USSN 08/772,330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1996
ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION: NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 317 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                       Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98101
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US-08-996-139-13
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                                                               184.5
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202.732 Million cell updates/sec
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Sequence 11, P
Sequence 11, P
Sequence 3, Ap
Sequence 2, Ap
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Sequence 13,
Sequence 4, A
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                                                                                           October 10, 2002, 12:48:46; Search time 38.1928 Seconds
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1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-052-521C-4
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Maximum Match 100%
Listing first 45 summaries.
                                                                 - protein search, using sw model
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Length 317

Score 1685; DB 4; Pred. No. 9.8e-164;

Mismatches

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241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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APPLICATION NUMBER: USSN 08/813,509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Immunex Corporation, STREET: 51 University Street
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                                                                                                                                                                 100.0%; Pr.
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                                                                                                                                                             100.08;
             ; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-995-659-13
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ZIP: 98101
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 317; Conservative
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(206)233-0644
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US-09-215-649A-13
 TELEFAX:
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                                       Gaps
                                                                                            1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQQV 60
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Patent No. 6242213
CENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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 Length 317;
                                       Indels
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d for Power Macintosh 6.0.1
; Score 1685; DB 3;
; Pred. No. 9.8e-164;
0; Mismatches 0;
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APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
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APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
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OPERATING SYSTEM: Apple Operating S
SOFTWARE: Microsoft Word for Power
CURRENT APPLICATION DATA:
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FILING DATE: 22 DECEMBER 1997
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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COMPUTER: Apple Power Macintosh
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
   100.0%;
100.0%;
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                    Similarity
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US-08-995-659-13
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Law Department

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180 HKVSLSSWYHDRGWAKISNWTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLM 239
VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
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                                                                                                                                                                                                                                                  Gaps
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APPLICANT: BOYLE, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-451BTV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
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Pred. No. 9.8e-164;
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100.0%; Pred. No. 9.8e-164;
iive 0; Mismatches 0;
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   REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                            TOPOLOGY: 11near

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13
                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09052521C Patent No. 6316408
                                                                                             NCE CHARACTERISTICS:
LENGTH: 317 amino acids
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ilarity 100.08;
Conservative 0
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Best Local Similarity 100.
Matches 317; Conservative
                                                                                                                           TYPE: amino acid
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Best Local Similarity
Matches 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Human
US-09-052-521C-4
                                                                                             SEQUENCE
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US-09-052-521C-4
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SEQ ID NO 4
LENGTH: 317
TYPE: PRT
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61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
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                                                                           Gaps
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                                                                                                                            1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ
                                                     QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICAM: BOYLE, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1417.5; DB 2
Pred. No. 1.9e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
84.1%; Score 1417.5;
Best Local Similarity 84.3%; Pred. No. 1.9e
Matches 268; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 316 amino acids
amino acid
                                                                                                                                                                                                                                                                                                          301 PDQDATYFGAGKVRDID 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
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119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL
                                                                                                                                                                                                                                                                                                                        APPLICANT: Boyle, William J. TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors FILE REFERENCE: A-451Brv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.9e-136; ; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.1%; Score 1417.5;
84.3%; Pred. No. 1.9e
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                         08/880,855
                                                                                                                                                                                                                                                               Sequence 2, Application US/09052521C Patent No. 6316408
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PRIOR FILING DATE: 1997-0
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SOFTWARE: Patentin Ver.
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APPLICANT: Anderson,
APPLICANT: Galibert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mouse US-09-052-521C-2
                                                                                                                                                                                                                                                 US-09-052-521C-2
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US-08-996-139-11
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 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
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                                                                                                                                                                                                                                                             Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 316;
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84.3%; Pred. No. 1.9e-136;
ive 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,090
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REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                       299 DPDQDATYFGAFKVQDID 316
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                                                                                                                                 300 DPDQDATYFGAFKVRDID 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-989-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Matches 268;
                                                                                                                                                                                                                                                US-08-989-362-2
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                 179
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NDMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/813,509 FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
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; Sequence 11, Application US/09215649A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2857
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
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amino acid
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Best Local Similarity 84.5%
Matches 250; Conservative
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MOLECULE TYPE: protein

US-08-995-659-11
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                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                           Seattle
                                                                                                                                                                      98101
                                                                                                                                                    COUNTRY:
                                                                                                         CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 GAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 KYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Indels
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
      CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.78; Score 1326.5; DB 3 84.58; Pred. No. 3.2e-127; ative 16; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
FRICA PAPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         UMBER: US/08/996,139
22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: PERKINS, PARTICLA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08995659
Patent No. 6242213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 294 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: MATASKOVSKY, Eugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 294 amino acids amino acid
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Best Local Similarity 84.5%
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-996-139-11
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     FILING DATE: 2:
CLASSIFICATION:
                                                                       Seattle.
                                                                                                              USA
                                                                                                                                 98101
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US-08-995-659-11
                                                                                                              COUNTRY:
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 CAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISE 81 202 SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGST 262 KYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID 317 ä Length 294; 78.7%; Score 1326.5; DB 4; Length 84.5%; Pred. No. 3.2e-127; Live 16; Mismatches 27; Indels

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APPLICANT: Michael R. Brigham-Burke
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: A METHOD OF IDENTIFYING RECEPTORS TRI AND TRZ
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT PILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 60/055,513
PRIOR APPLICATION NUMBER: 60/056,980
PRIOR PILING DATE: 1997-08-26
PRIOR PILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 ODTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 -DSYWDPNDEESMNSPCWQVKW-----OLRQLVRKMILRTSEETI-----STVQEKQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 LEAQPF-----AHLT----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMYYVTKTSIKIPSSHTLMKGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 RNSCWSKDAEYGLYSIXQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Kathryn A. Anderson, Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 1.4e-17; 61; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 ^{\rm H}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/670,354
25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08670354 Patent No. 5763223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%;
24.1%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.99
Best Local Similarity 24.13
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CY NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-072-993C-3
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AEKAMYDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGST 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 GAPHEGPLH-APPPAPHQPPAASRSMFVALLGLGLGQVVCSVALFFYFRAQMDPNRISE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 KYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 294;
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION NUMBER: US/09/215,649A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                               TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.7%; Score 1326.5; DB 4; Best Local Similarity 84.5%; Pred. No. 3.2e-127; Matches 250; Conservative 16; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <UDKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/72,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-09-215-649A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-Dec-1998 CLASSIFICATION: <Unknown>
                                                                            Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                 CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202
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APPLICATION NUMBER: FILING DATE: 25-JUI

RESULT 11 US-09-072-993C-3

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200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
                                                                                                                                                                                                                                                                                             168 HLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDFILLMKSA 226
                                                                          100 ODTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAERAMVDGSWLDLARRSR 159
                                                                                                                                                                                                       108 ONISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
                                                                                                       62. -DSYWDPNDEESMNSPCWQVKW------QLRQLVRKMILRTSEETI-----STVQEKQ 107
                                                                                                                                                                 ---AHLT----INATDIPSGSHKVSL----SSWYHDR-GWAKLSNM 199
               260 STKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDATYFGAFKV 313
                                                                                                                                                                                                                                                                                                                                                                   227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV, 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08780496 Patent No. 6046048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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                                                                                                                                                                        160 LEAQPF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 QDTTLESQDTKLIPDSCRRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 LEAQPF-----AHLT----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKED---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.9%; Score 251.5; DB 1; 24.1%; Pred. No. 1.4e-17; Live 61; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 14.9%; Score 251.5; DB 3; Best Local Similarity 24.1%; Pred. No. 1.4e-17; Matches 71; Conservative 61; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION 1 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
ATTORNEY/APPRIOR: 435
ATTORNEY/APPRIOR: 11
                                                                                                                                                                                                                                                                32,172
P· 2835-B
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TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,17;
REFERENCE/DOCKET NUMBER: 28
FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
                                                                                                                                                                                                                                                                                                                                                                         TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               (206) 587-0430
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 281 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 24.18
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-670-354-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-08-584-031-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --AHLT----INATDIPSGSHKVSL----SSWYHDR-GWAKISNM 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 PSLGQTCVLIVIFTVLLQSLCVAVTYVFTNELKQMQDKYSKSGIACF----LKED--- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.9%; Score 251.5; DB 3; Best Local Similarity 24.1%; Pred. No. 1.4e-17; Matches 71; Conservative 61; Mismatches 117;
               MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      SOFTWARE: WinPatin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFTCATION: 435
                                                                                                                                                                                                                                         NAME: Marschang, Diane L. REGISTATION NUMBER: 35.00 REFERENCE/DOCKET NUMBER: P00 RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 amino acids
                                                                                                                                                                                                                                                                                                                                                                415/952-9881
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COMPUTER READABLE FORM:
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                                         200 TFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259
                                                                 108 QNISPLVRERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 PAASRSMFVALLGLGLGQVVCSVALFFYFRAQMD--PNRISEDGTHCIYRILRLHENADF 99
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                                                                                                                                        227 RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 281;
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MEMBER OF THE THE FAMILY USEFUL TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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61; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.9%; Score 251.5; 24.1%; Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VETSION 2.0
SOFTWARE APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                   Sequence 10, Application US/08883086
Patent No. 6171787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porembski, Priscilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 61
FELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: NO. 6171787e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: : | :: | :: | 62 -DSYWDPNDEESMNSPCWQVKW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                   STEVEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
IOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: FASTSFG
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: WILEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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October 10, 2002, 12:48:46; Search time 4.02108 Seconds (without alignments) 414.343 Million cell updates/sec OM protein - protein search, using sw model 1 OYIKANSKFIGITEL 15 US-09-787-126-34 74 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 seqs, 111073796 residues rched:

747574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_032802:* Database :

/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* DAT .DAT: DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT: /gcgdata/geneseg/genesegp-embl/AA1989 /gcgdata/geneseg/genesegp-embl/AA1996 /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980. /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981. /gcgdata/geneseq/geneseqp-embl/AA1993 /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994 /SIDS1/gcgdata/geneseqy-emb1/AA1995 /SIDS1/gcgdata/geneseqy/geneseqp-emb1/AA1996 /SIDS1/gcgdata/geneseqy/geneseqp-emb1/AA1996 /SIDS1/gcgdata/geneseq/geneseqp-embl /SIDS1/gcgdata/geneseq/geneseqp-embl /SIDS1/gcgdata/geneseg/genesegp-/SIDS1/gcgdata/geneseqp

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	•	Description	, Tetanus toxin epit	Universal T-cell e	Tetanus toxoid uni	Tetanus toxin frag	Universal helper T	T-Helper epitope f	T-cell epitope pep	Tetanus toxoid epi	Tetanus P2 epitope	Tetanus toxoid T c	Foreign epitope P2
		CI.	AAR06310	AAW35506	AAW11505	AAW67033	AAW71321	AAY04051	AAW67578	AAW73220	AAB45511	AAY82637	AAY92625
			11	18	18	19	19	20	20	20	21	21	21
		Match Length DB	15	15	15	15	15	15	15	15	15	15	15
æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	74	74	74	74	74	74	74	74	74	74	74
	Result	NO.	н	7	m	4	Ŋ	9	7	80	σ	10	11

ALIGNMENTS

AAR06310 standard; protein; 15 AA. 04-DEC-1990 (first entry) retanus toxin epitope. AAR06310; RESULT 1 AAR06310

Tetanus toxin; vaccine; major histocompatibility complex; MHC; antimalarial.

Synthetic.

25-JUL-1990. 3P378881-A.

89EP-0203318. 89IT-0022409. 89IT-0019110. 27-DEC-1989; 16-NOV-1989; 17-JAN-1989; (ENIE) ENIRICERCHE SPA.

Pessi A, Bianchi E, Verdini AS, Corradin G;

WPI; 1990-225582/30.

Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used as universal carriers for prepn. of immunogenic conjugate(s) for use as vaccines.

us-09-787-126-34.rag

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AAW11505;
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                                                                                                                                                                                                                                                                              RESULT 3
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through a linker to a solid phase, forming a complex of (A)-solid phase.

Where (A) comprises 10-50 amino acids capable of forming a secondary structure in a benigh buffer after liberation from the solid phase, and turther the (A)-solid phase complex comprises an immunogenic substance and/or an immune mediator coupled on (A). The present sequence composents a peptide used in an example from the present invention. An represents a peptide used in an example from the present invention of chemical derivatives, characterised by covalently attaching molecules at attachment points. Alternatively (A) is used as a scaffold peptide for the incorporation into an Immunostimulating Complex (Iscom) resulting an (A)-iscom complex which is used for the chemical coupling of antigenic substances in an aqueous solution by conjugation. (A) derivatised with higher applies having fibronectin., laminin. Or vitronectin-like the production of the chemical coupling of antigenic continue and the new constant the most of the chemical coupling of antigenic constant the most of the chemical coupling of antigenic constant the most of the chemical coupling of antigenic constant the most of the chemical coupling of antigenic constant the most of the chemical coupling of the chemical coupling of antigenic constant the most of the chemical coupling of the chem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour; scaffold; inhibition; metastasis; wound healing; solid phase.
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-dendritic peptide carrier linked to a solid phase - useful as a
                               Epitopic peptides may be used with synthetic hapten derived from a pathogen to generate an immune response to the pathogen. Peptides are recognised by numerous Thelper cell clones within the context of a wide range of alleles of the human MHC. The peptides may be used in an antimalarial vaccine inducing Ab. response to P.falciparium.
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                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                        DB 11;
3.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Universal T-cell epitope peptide SEQ ID NO:8.
                                                                                                                                                                                                    Score 74; DB Pred. No. 3.3 ; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAW35506 standard; peptide; 15 AA.
   Claim 1; Page 17; 20pp; English
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                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                  1 QYIKANSKFIGITEL 15
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                                                                                                                                                                       15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                         Sequence
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agent. Such diagnostic-(A) molecules could be used to detect molecules derived from or indicative of pregnancy or of a disease, such as an infectious, autoimmune or cancerous disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic DNA coding for the wild-type universal Th epitope from tetanus toxoid, designated TT830, was fused to the 3'-end of DNA encoding heavy chain sequences from the humanised anti-Fc gamma RI monoclonal antibody H22. The resulting fusion protein was shown to be significantly more efficient in antigen presentation and T cell stimulation that the TT830 epitope alone. A similar fusion construct was prepared coding for a mutant, antagonistic form of the epitope (designated TT8335) fused to the anti-Fc gamma RI. The Inhibiting T cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific; fusion protein; chimera; tetanus toxoid; helper T cell epitope; antigen presentation; ds.
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant, multi-specific anti-Fc receptor antibody molecules also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection
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                                                                                                                                                             Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 74; DB 18;
100.0%; Pred. No. 3.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                        . 100.0%; Score 74; DB 18;
ilarity 100.0%; Pred. No. 3.3e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetanus toxoid universal Th epitope TT830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graziano R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Fig 24; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW11505 standard; Protein; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OYIKANSKFIGITEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium tetani.
                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
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                                                                                                             Sequence 15 AA;
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Local Simi
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W09948925-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrimeric poly-lysine enabling multiple eptitopes to be covalently attached to it. Also claimed are: (1) an antibody purified from biological fluid or cells of organisms administered with the carbohydrate peptide conjugate, and (2) a diagnosis kit comprising antigen-specific antibodies elicited by immunisation with the carbohydrate peptide conjugate. The peptide conjugate, antibody and diagnosis kit are used to provide pharmaceutical compositions and vaccines against tumours. These can be used to support an immune response against viral infections caused by hepatitis virus, HIV or cytomegalo virus. They can be used to enhance immune responses, especially B- and reall responses, of humans and animals against bacterial infections. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carbohydrate peptide conjugate stimulates the antibody and T-cell response without stimulating undesired immune responses. The composition is capable of increasing the survival of tumour bearing humans and animals. The present sequence corresponds to residues 830-844 of tetanus toxin. The synthetic peptide corresponding to this sequence may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                  Carbohydrate peptide conjugate used as vaccine - comprises carrier with dendrimeric poly-lysine enabling multiple epitopes to be covalently attached
                                                                                                                         Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate; dendrimeric poly-lysine; epitope; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as an epitope in a carbohydrate peptide conjugate.
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                                                                                                                                                                                                                                                                                                       Lo-man R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                     Tetanus toxin fragment (residues 830-844).
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                                                                                                                                                                                                                                                                                                      Leclerc C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW71321 standard; peptide; 15 AA.
                                 AAW67033 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                      Cantacuzene D,
                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR.
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Best Local Similarity
                                                                                                                                                              Clostridium tetani.
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                                                                              15-DEC-1998
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                                                        AAW67033;
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          RESULT 4
AAW67033
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AAW71321-22 represent universal helper T-cell epitopes derived from tetanus toxin. They are used to enhance host immune response to vaccines. The specification describes a plasmodium yoelil liver stage 17 kba hepatic and erythrocytic stage protein designated PyHEPI. This protein elicits a response from an Igl monoclonal antibody designated say Yoelil Liver Stage 3 (NTLS3). This antibody does not recognise sporozoites, but does recognise P. yoelil liver stage parasites. NTLS3 eliminates upto 90% of liver stage parasites. The specification describes a vaccine for reducing the severity or incidence of infection by a malaria parasite of the PyHEPI7 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine for protecting mammal against infection by malaria caused by Plasmodium species - comprises a first nucleic acid encoding a first polypeptide capable of eliciting an immune reaction against an antigen expressed during the liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                 Liver stage, Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3; hepatic and erythrocytic stage protein; PyHEP17; vaccine; malaria parasite; teanus toxin; P2; helper T cell epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Iniversal helper T-cell epitope P2 derived from tetanus toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 74; DB 19;
100.0%; Pred. No. 3.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hedstrom RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 12; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY04051 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0319704.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charoenvit Y, Doolan DL,
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                         Synthetic.
Clostridium tetani.
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                                                                                                                                                                                                                                                                                                                                                                                                                       07-0CT-1994;
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Gaps

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30-SEP-1999

Paul S,

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This sequence represents a tetanus toxoid epitope and is recognised by the multispecific single chain antibody designated H22. The antibody can be used in the method of the invention for inducing antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell which is characterised by overexpression of HER 2/neu or epidermal growth factor receptor (EGFR), comprises contacting the tumour cell with a multispecific protein molecule (preferably a single chain antibody) comprising: (a) an anti-Fc receptor antibody or an antigen binding fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which binds to HER 2/neu; and (c) a portion which binds to HER 2/neu; and (c) a portion which binds to HER 2/neu; and (c) a portion which
                                                                                                                                            The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused via a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a T-cell epitope peptide used to generate the chimeric peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multispecific single chain antibody; antibody H22; tumour cell; therapy; antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Specific killing of tumour cells - using a multi-specific molecule comprising an anti-Fc receptor antibody and a portion which binds to a target cell
                                                            Synthetic chimeric fimbrin peptide – useful for vaccination against non-typable Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu epidermal growth factor receptor; breast cancer; ovarian
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                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 74; DB 20; 100.0%; Pred. No. 3.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                  Disclosure; Column 4; 16pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW73220 standard; Protein; 15 AA.
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retanus toxoid epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDA-) MEDAREX INC.
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                                                                                                                                                                                                                                                                                                                                                15 AA;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses new covalently reactive antigen analogs (CRAA) of formula X1-Y-E-X2, in which X1 and X2 represent peptide sequences of an epitope of a disease-associated protein, Y is a positively charged amino acid residue, preferably Lys or Arg, and E is an electrophilic reaction centre, preferably Lys or Arg, and E is an electrophilic reaction centre, preferably a phosphonate or boronate moiety. Depending on the identity of the epitope, the CRAA may be used to stimulate production of catalytic antibodies specific for predetermined antigens associated with particular medical disorders. They may also be used to permanently inactivate endogenously produced catalytic antibodies produced in certain autoimmune diseases as well as in certain lymphoproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421-436 of a B-cell epitope of gp120 (see AAY04046) which may be used to counter HIV-1 infections. When used as an immunogen, preferably this CRA is conjugated at its N-terminal to a T-helper epitope from tetanus toxoid. The present sequence represents the T-helper epitope and
                                                                                                                                                                                                                                                                            New covalently reactive antigen analogs used for treating e.g. autoimmune diseases, lymphoproliferative disorders, cancers, microbial infections, ischemic and reperfusion injury or septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 74; DB 20; ilarity 100.0%; Pred. No. 3.3e-07; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponds to residues 830-844 of the toxoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogenic composition; immune response.
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 86; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW67578 standard; peptide; 15 AA.
                                                                                                                                                                                   Smith L;
                                           99WO-US06325.
                                                                                         98US-0046373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OHIS ) UNIV OHIO STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYIKANSKFIGITEL 15
                                                                                                                                                                                     Gololobov G,
                                                                                                                                       (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                 WPI; 1999-591076/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AA;
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                                                                                       23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5843464-A
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Sequence

3888888888888**%**&

Query Match

01-DEC-1998

AAW67578;

AAW67578 RESULT 7

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r cell epitope; B cell epitope; allergy; allergen; antigenic; antiallergic; antiathmatic; antiinflammatory; dermatological; ammunosuppressive; vaccine; rhinitis; sinusitis; bronchial asthma; atopic dermatitis; accine urticaria; chronic urticaria; gastro-intestinal syndrome; food allergen; oro-pharyngeal syndrome
                                                                                                                                                     Tetanus toxoid I cell epitope peptide SEQ ID NO:13.
                    AAY82637 standard; peptide; 15 AA.
                                                                                                             07-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                   AAY82637;
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AAY 82637

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  breast cancer or ovarian cancer. The multispecific antibody can also be administered prophylactically to vaccinate a subject against infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eosinophilia, allergic rhinitis and other allergic diseases. These involve the use of interleukin-5 (IL-5) analogues and modified IL-5 proteins and their coding sequences to down-regulate IL-5 activity and thus reduce eosinophil numbers. The allergic diseases may be treated using autovaccines, nucleic acid vaccines or live vaccines. In addition, it is possible that they may be used in the treatment of cancer and helminthic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asthma; IL-5; interleukin-5; allergy; cytokinė; helminthic infection; cancer; eosinophilia; vaccine; allergic rhinitis.
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention is concerned with methods of treating asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Down-regulating interleukin 5 (IL-5) activity in humans by administering IL-5 and/or an IL-5 analogue, useful in the treatm prophylaxis or amelioration of asthma or other chronic allergic conditions
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                                                                                                                                    Length 15;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 74; DB 21;
100.0%; Pred. No. 3.3e-07;
ive 0; Mismatches 0;
                                                                                                                                  Score 74; DB 20;
Pred. No. 3.3e-07;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 137; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    AAB45511 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetanus P2 epitope SEQ ID NO: 23.
                                                                                                                                                                                 ;
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                                                                                                                                    100.0%;
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99US-0132811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                    1 QYIKANSKFIGITEL 15
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
                                                by a target cell.
                                                                                          15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              AAB45511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food allergens, oro-pharyngeal syndrome, anaphylactic reactions associated with drug hypersensitivities and/or a mixture of these. The use of (I) in the treatment of allergic conditions avoids the need for drug treatment, which often causes undesirable side-effects. Also, prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compound for prevention and treatment of allergies comprises at least one allergen antigenic determinant recognized by a B cell and at least one antigenic determinant which does not trigger T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 art drug therapies alleviate symptoms, but do not influence their causes, however (I) actually combats the cause of an allergic reac
The present sequence represents a peptide, which is used in an
anaphylactic reaction; drug hypersensitlyity; allergic reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                 99WO-BE00092
                                                                                                                                                                                                                                                                                                                                                                                     98EP-0870167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saint-Remy J, Jacquemin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-422470/36.
                                                                       Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                       WO20006694-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIO ) UCB SA
                                                                                                                                                                                                                                                                                                                 20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activation
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Gaps

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Indels

Conservative

QYIKANSKFIGITEL 15 1 QYIKANSKFIGITEL 15

ð g RESULT 10

Foreign epitope P2.

10-AUG-2000

AAY92625;

AAY92625

Clostridium tetani

WO200020027-A2

05-OCT-1999;

13-APR-2000.

20-0CT-1998; 05-0CT-1998;

Steinaa L, Gautam A,

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The present sequence represents the tetanus toxoid P2 epitope. It is used to create a fusion protein with murine osteoprotegerin ligand (10PGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OpCL protein is synthesised as a type II cansmembrane protein. The murine and human OpCL polypeptides are 87% homologous. OpCL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast conformation in the absence of CSF-1. OpCL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-requisation of OpCL activity in an animal. The method comprises down-requisation of OpCL polypeptide or subsequence, and/or at least one OpCL polypeptide are useful for treating, preventing and ameliorating contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant protein; CDC/NIIMALVAc-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
                                        Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium tetani tetanus toxoid T-cell epitope, P589.
Amino acid sequence of the tetanus toxoid P2 epitope.
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100.0%; Pred. No. 3.3e-07;
ive 0; Mismatches 0;
                                                                                                                  osteoporosis; bone resorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to treat, prevent and ameliorate osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Page 106; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                     98DK-0001164.
                                                                                                                                                                                                                                                                                                                           . 99WO-DK00481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                        tetanus toxoid P2 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QYIKANSKFIGITEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-271444/23.
                                                                                                                                                                                          Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
                                                                                                                       immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone resorption
                                                                                                                                                                                                                                  WO200015807-A1.
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                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                             13-SEP-1999;
                                                                                                                                                                                                                                                                                  23-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenic cell-associated peride antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foreign to the animal. Analogues of human PSM, human Her2 and human/muthe FGPB comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope (e.g. P2 and/or P30) are also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The claims detail a method for inducing immune responses against weakly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                  Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2; Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nielsen KG, Haaning J, Leach D, Dalum I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 74; DB 21;
100.0%; Pred. No. 3.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 213; 220pp; English.
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                                      AAY92625 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       en S, Niels
Karlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98DK-0001261.
98US-0105011.
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1 QYIKANSKFIGITEL 15
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N-PSDB; AAA09460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
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Gaps

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15 AA;

Sequence

SXC

AAY84427;

AAY84427 ID AAYE XX AC AAYE XX DT 25-5

RESULT 12

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Length 15; Indels

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                                                                                                                                                                                                                                                                                                          The present sequence is the tetanus toxoid T-cell epitope P589, derived from Clostridium tetani. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSP-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface layer protein; S-layer secretion signal; antibiotic; vaccine; recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff; antibacterial enzyme; surface glycoprotein; T-cell activating epitope; P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.
EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                      Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetanus toxoid protein derived T-cell activating epitope P2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 74; DB 21;
100.0%; Pred. No. 3.3e-07;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting P. falciparum in biological samples
                                                                                                                                                                    US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY44763 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                         Claim 2; Page 17; 52pp; English.
                                                                                                                                                                                           Shi YP, Hasnain SE;
                                                                                                         99WO-US18869.
                                                                                                                                98US-0097703
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Matches 15; Conserv
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                                      Clostridium tetani.
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                                                           WO200011179-A1.
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                                                                                                                                  21-AUG-1998;
                                                                                                          19-AUG-1999;
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                                                                                   02-MAR-2000
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The patent discloses a method for cleaving a recombinant fusion protein which is produced by Caulobacter and consists of Caulobacter surface which is produced by Caulobacter and consists of Caulobacter surface layer (S-layer) protein (containing the C-terminal secretion signal) and a target protein protein is carried out under mild acid conditions so that cleavage occurs at aspartate-proline dipeptide site without solubilising the protein. The Caeavage is accomplished while the fusion protein is in an insoluble aggregate form which facilitates purification of the protein. The method is useful for producing pure proteins including recombinant human and animal therapeutic antiblotic and vaccine peptides, enzymes, protein polymers, and antibacterial enzymes for foodstuffs.

The present sequence is a T-cell activating epitope P2 derived from tetanus toxold protein. This sequence was fused to a DNA encoding a from tetanus toxold protein. This sequence was fused to a DNA encoding a fragment of Infectious pancreatic necrosis virus surface glycoprotein which is a vaccine candidate. This chimeric protein was in turn fused to DNA encoding C crescentus S-layer secretion signal (corresponds to the C-terminal portion of the S-layer protein from amino acid 690 onwards and contains native Asp-Pro site) for construction of a recombinant contains native which is expressed in Caulobacter and then cleaved
                                                                                                                                                                                                                                                                                                                                                         Cleavage of Caulobacter produced recombinant fusion proteins useful for producing vaccine peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amyloid protein; neuroprotective; nootropic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease; anticonvulsant; gene therapy; Pick's disease; antidiabetic; systemic amyloidosis; maturity onset diabetes; ALS; amyotrophic lateral sclerosis; Parkinson's disease; encephalopathy; Huntington's disease; fronto-temporal dementia; P2 epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 16; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE11763 standard; peptide; 15 AA.
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                                                                                                                                              UYBR-) UNIV BRITISH COLUMBIA.
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99WO-CA00637
                                                                        98CA-2237704
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                            14-JUL-1998;
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Birk P, Jensen MR, Nielsen KG;
01-MAR-2000; 2000US-186295P.
        (MEBI-) M & E BIOTECH AS.
                          WPI; 2001-589796/66.
N-PSDB; AAD18755.
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The invention relates to a method for in vivo down-regulation of amyloid protein such as beta amyloid (Abeta) in an animal, including human. The In vivo down-regulation of amyloid protein for the treatment of Alzheimer's v. comprises presenting an amyloidogenic polypeptide or its subsequence and/or at least one analogue of the amyloidogenic polypeptide to the immune system Example 3; Page 117; 120pp; English.

method comprising presenting to the animal's immune system an immunogenically effective amount of at least one amyloidogenic protein or its subsequence and/or at least one analogue of the amyloidogenic protein or its subsequence, and its polypeptide. The amyloidogenic protein or its subsequence, and its analogue is useful for the preparation of an immunogenic composition comprising an adjuvant for down-regulating amyloid in an animal. They are also useful in the treatment, prophylaxis or amelioration of Alzheimer's disease or other diseases characterised by amyloid deposits. They are also useful in the treatment of systemic amyloidosis, maturity onset diabetes, Parkinson's disease, Huntington's disease, fronto-temporal dementia, amyotrophic lateral sclerosis (ALS), pick's disease and prion-related transmissable spongiform encephalopathies. They are also useful for inducing production of antibodies against an amyloidogenic polypeptide. The present sequence is clostridium tetani P2 epitope related to the invention

15 AA Sequence

Gaps ö Length 15; Indels Query Match 100.0%; Score 74; DB 22; Best Local Similarity 100.0%; Pred. No. 3.3e-07; Matches 15; Conservative 0; Mismatches 0;

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1 OYIKANSKFIGITEL 15

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1 QYIKANSKFIGITEL 15

Search completed: October 10, 2002, 16:00:56 Job time : 5.02108 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
OM protein - protein search, using sw model
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Run on: October 10, 2002, 12:48:46; Search time 1.76205 Seconds (without alignments)
329.613 Million cell updates/sec Title: US-09-787-126-34
Perfect score: 74
Sequence: 1 QYIRANSKFIGITEL 15

Sequence: 1 QYIKANSKFIGITEL 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

irched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters:

ocal number of nics sacisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P04958 clostridium							٠.		_		Q9cev7 lactococcus		_	_	066922 aquifex aeo					-	Q09325 rattus norv		-	-				-			077 rhodoba	Fil410 pichia jadi
COTTANDA	a	TETX_CLOTE	VG84_BPML5	MSP1_PLAF3	MSP1_PLAFF	MSP1_PLAFM	MSP1_PLAFC	MSP1_PLAFP	PYRC_SERMA	V120_HSVSA	ACPD_HAEIN	PEF1_LACLC	PEPF_LACLA	YHJ9_YEAST	KAD_MYCCA	YD83_METJA	TRUB_AQUAE	HEMA_PI3HT	Y096_HAEIN	GNT1_HUMAN	GNT1_MOUSE	GNT1_RABIT	GNT1_RAT	Y032_BORBU	G6PD_ASPNG	G6PD_EMENI	YDD2_SCHPO	Y358_BUCAI	MIP_CHLPN	YD01_CLOAB	DPOB_XENLA	MURD_BACSU	NIFN_RHOCA	G6PD_PICJA
dР	Query Match Length DB	100.0 1314 1	59.5 66 1		_	57.4 1701 1	7.4	₹.	55.4 204 1	₹.	۲.	٦.	54.1 601 1	_	7	*	<#	₹.	0	0.	0	0.		0.			0.	9.	.و	9.	9.	9.	48.6 461 1	48.6 495 1
	Result No. Score	1 74	2 44	3 42.5	4 42.5	5 42.5	6 42.5	7 42.5	. 8 41	9 41	10 40	11 40	12 40	13 40	14 39	15 38	16 · 38			19 37	20 37	21 37	22 37	23 37	24 37	25 37	26 37	27 36	. 28 36	29 36	30 36	31 36	32 36	33 30

P40009 saccharomyc P21770 influenza c P13877 influenza c P04932 plasmodlum P04933 plasmodlum Q9m318 spinacia ol P04354 gallus gall P13652@escherichia Q10494 schizosacch P25415 emericella P17212 lactobacill P24872 equine herp	14 AA. date) update) (Tentoxylysin). dium group; Clostridiaceae;	chen A., Engels J., nn H.; ssion in E. coli, and	tetanus toxin."; d D.J., Allen G., Thomson R.O.; expression of tetanus toxin	, Habermann E.; positions of sulfhydryl groups positions of sulfhydryl groups	Benfenati F., Tauc L., its inhibition of activity depend on zinc.";
YNDI_YEAST RRP3_INCBE RRP3_INCJJ MSP1_PLAFK MSP1_PLAFK MSP1_PLAFK MSP1_PLAFK MSP2_SPOL CGBV_CRICK CDD_ECOLI YGG7_SCHPO DHQA_EMENI ALIXD_LACHE VGLD_HSVEA	PRT; 131. ed) sequence upd nnotation u 3.4.24.68)	36478; tzki K., Benschen, ann E., Niemann H. ucture, expression ins.";	; e of 1986) ickar and ;	DS. Turi	, O., and tease
630 1 774 1 1630 1 1630 1 176 1 294 1 329 1 329 1 329 1	μ, υ	FROM N.A. 87053814; PubMed=3536478; 7, Jarausch W., Goretzki K., 7, Hudel M., Habermann E., 7, Foxin: primary structure, with botulinum toxins."; 5:2495-2502(1986). FROM N.A.	40747; PubMed=3774 NF., Lyness V.A. te nucleotide sequesses. 14:7809-78 742-1314 FROM N.A. 85672; PubMed=3510 NF., Lyness V.A. ucleotide sequenci in Escherichia col	; AND DISULFIDE BC ; PubMed=2108021; Henschen A., Welle disulfide bridges ["; 188:39-45(1990). ; PubMed=1935979; ; Henschen A.H., Welle ysis of tetanus tc, f cleavage sites. f cleavage sites. f 202:41-51(1991).	e D D C
44444444 8888 98	(Re (Re (Re tet tet tet tet tet tet tet tet tet t	E FROM N.A. -87053814; Pubm -, Jarausch W., U., Hudel M., H s toxin: primar y with botulinu j 5:2495-2502(19 E FROM N.A.	40747; N.F., te nuc ds Res 742-1: 85672; N.F., ucleot in Escl	UENCE, K., H. t. of d. t. of d. toxin. chem. UENCE. UENCE. R.G., oteoly	TION AS ZI 110948; Pt. Poulain C.; exin is a
	LOTE ETX_CLO 04958; 04958; 3-AUG-1 5-JUL-1 etanus lostrid 1asmid. lasmid. lasmid.	[1] SEQUENCE FROM N.A SEQUENCE—87053814; EISEL U., Jarausce Weller U., Hudel "Tetanus toxin: phomology with bort EMBO J. 5:2495-25 [2] [2] SEQUENCE FROM N.A STRAIN—CRI3911;	MEDLINE-87040747; PubMed-3774547 Faliweather Nr., Lyness V.A.; "The complete nucleotide sequency Nucleic Acids Res. 14:7809-7812([3] SEQUENCE OF 742-1314 FROM N.A. MEDLINE-86085672; PubMed-3510187 Faliweather Nr., Lyness V.A., P. "Cloning, nucleotide sequencing, fragment C in Escherichia coll." 1. Bacteriol. 165:21-27(1986).	PARTIAL SEQUENCE, AND DISULFIDE BON MEDLINE-90201034; PubMed-2108021; Krieglstein K., Henschen A., Weller "Arrangement of disulfide bridges at tetanus toxin."; Bucchen. 188:39-45(1990). [5] PARTIAL SEQUENCE; PubMed-1935979; MEDLINE-92037649; PubMed-1935979; Krieglstein K.G., Henschen A.H., We "Limited proteolysis of tetanus tox identification of cleavage sites."; I Riochem. 202:41-51(1991).	IGNO TO
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829 QYIKANSKFIGITEL 843
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                                                                                    VG84_BPML5 :
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                                                                                                                                                                                                                             DELECTION.";

Nat. Struct. Biol. 4:788-792(1997).

-I FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

-I FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

WHERE IT CAN MOVE BETWEEN PROSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GIN-|-PHE-77
                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE AND ARE NON-TOXIC AFTER SEPARATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
                                             MEDLINE-93063293; PubMed-1331807; Schlavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Schlavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Mosqupta B.R., Montecucco C.; "Tetanus and botulinum-B neurotoxins block neurotransmitter release
                                                                                                                                                                                    Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANBOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO GANGLIOSIDE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-|-PHE-77 BOND IN
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                                                                                                                                                                                                                     Structure of the receptor binding fragment HC of tetanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150550 MW; 134C3657133EF81D CRC64;
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TETANUS TOXIN HEAVY CHAIN.
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                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
                                                                                                             proteolytic cleavage of synaptobrevin.";
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InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
                                                                                                                                                                       MEDLINE-97475217; PubMed-9334741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X04436; CAA28033.1; --
EMBL; M12739; AAA23282.1; --
EMBL; X06214; CAA29564.1; --
PIR; A25689; BTCLTN.
PDB; 1AF9; 29-APR-98.
PDB; 1A8D; 14-OCT-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00760; BONTOXILYSIN.
                              IDENTIFICATION OF SUBSTRATE
EMBO J. 11:3577-3583(1992).
                                                                                                                           Nature 359:832-835(1992).
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                  "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Certa U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen
precursor pl90 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tolle R., Bujard H., Cooper J.A.; Plasmodium falciparum: variations within the C-terminal region of
                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 66;
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Pred. No. 0.21;
                                                                                       update)
66 AA.
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PRT;
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-9321128#; Pubmed-8459766;
MEJLINE-9321128#; Skris G.J.;
Matfull G.F., Skris G.J.;
**DNA sequence, structure and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-1061 FROM N.A. MEDLINE-88166657; PubMed=3327688;
                                              Created)
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Local Similarity 57.1%;
nes 8; Conservative
STANDARD;
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                                                                                                            Gene 84 protein (GP84).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                       01-FEB-1994 (Rel. 28, 01-FEB-1994 (Rel. 28, 01-FEB-1994 (Rel. 28,
                                                                                                                                                        Mycobacteriophage L5
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NCBI_TaxID=5834;
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P19598; Q25921;
01-FEB-1991 (Re.
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Conservative:

Matches

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(Potential).

PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88142999; PubMed-2449612; Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.; Wariation in the precursor to the major merozoite surface antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 27:291-302(1988).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential).
PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDa, KDa AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OIM MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEMBRANE ANCHOR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID-5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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60.0%;
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                                                                                                                                                                                                                                                                                                     GPI-anchor
                                                                                                                                                                                                              CAA68280.1;
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983 QFVKSNSKVITGLTE 997
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1178 117
1569 156
1682 AA;
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                      Transmembrane;
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P13819;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Merczolte surface protein 1 precursor (Merczolte surface antigens)
(PMMSA) (P190)

    -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor

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Plotymorphism of the precursor for the major surface antigens of
Plosmodium falciparum merozoites: studies at the genetic level.";
EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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MEDLINE-86136024; PubMed-3004972;
Mackay M., Goman M., Bone N., Hyde J.E., Scalfe J., Certa U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum (isolate mad20 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70153;
                                                                                                                                                                                                          POTENTIAL. MEROZOITE SURFACE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              1701 AA; 193719 MW; 3920B75E73D38552 CRC64;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                     EMBL; M19143; AAA29653.1; -.
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SIGNAL
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P08569;
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                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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MEDLINE-8814399; PubMed-3278296;
Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
Werozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 16:1206-1206(1988).
           PTM: MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa and 19 kDa antigens which are the major surface antigens of merozottes. The maturation take place during schizont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-0CT-1996 (Rel. 34, Last annotation update)
Merozolte surface protein 1 precursor (Merozolte surface antigens)
(PMMSA) (P195).
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MEDLINE-86205236; PubMed-3517809;
Weber J.L., Leininger W.M., Lyon J.A.;
Variation in the gene encoding a major merozoite surface antigen the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 14:3311-3323(1986).
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Pred. No. 11;
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60.0%;
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1001 QFVKSNSKVITGLTE 1015
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Best Local Similarity 60.0.
Best Local 9; Conservative
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PIR; B25120; B25120.
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 (Potential)
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P04934;
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PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa MAD 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                        (Potential).

PTM: MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 4 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SUBRACE ANTIGENS OF MEROZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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Exp. Parasitol. 67:1-11(1988).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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major merozoite surface antigen (gpl95) of the Uganda-Palo Alto
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Transmembrane; GPI-anchor.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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MEDLINE-89005525; PubMed-3049134;
Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
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MEROZOITE
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
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MSP1_PLAFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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(POTENTIAL)
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                                                                                                                                                                            Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 5B59CEEFA2F9A026 CRC64;
                                                                                                                                                                                                                       PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
114-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                       MEROZOITE SURFACE
                                                                                                                                                                                                                                  N-LINKED (GLCNAC,
                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AA.
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Pred. No. 12;
4; Mismatches
                                                                                                                                                                                                         POTENTIAL
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N-LINKED
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                                                                                                                                              InterPro; IPR000561; EGF-11ke. Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  196174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1026 QFVKSNSKVITGLTE 1040
                                                                                                                                EMBL; M37213; AAA29611.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QYIKANSKFI-GITE 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aspartate.
                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SM6;
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Q9S3S1;
                                                                                                                                                                                                                       CHAIN
CARBOHYD
CARBOHYD
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the Euro
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92333688; PubMed-1321287; Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B., Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                   Score 41, DB 1; Length 204;
Pred. No. 2.4;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of the herpesvirus saimiri genome.";
                                                                                                                                            2,04 AA; 22899 MW; 9DB0B6C9B834B310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpesvirus saimiri (strain 11).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1;
Pred. No. 11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                      EMBL; AF175466; AAD50307.1; ALT_INIT.
Interpro; IPR002192; Dilydrocratase.
PROSITE; PS00482; DIHYDROOROTASE 1; PARTIAL.
PROSITE; PS00483; DIHYDROOROTASE_2; 1.
                                                                                                                                                                                                                                                                                                                               899 AA
                                                                                                                Pyrimidine biosynthesis; Hydrolase; Zinc. NON_TER 1 1 SEQUENCE 204 AA; 22899 MW; 9DB0B6C9B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X64346; CAA45686.1; -..
EMBL; M86409; AAA46139.1; -..
PII;, G36812.
Capsid assembly.
SEQUENCE 899 AA; 103350 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%;
                                                                                                                                                                      55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Virol. 66:5047-5058(1992)
                                                                                                                                                                                                                                                                                                                                                                                                     Capsid assembly protein 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 50.v.
7; Conservative
                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                          42 OYVQAGNRELGAT 54
                                                                                                                                                                                                                                1 QYIKANSKFIGIT 13
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     63 OR EERF1.
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Q01055;
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V120_HSVSA
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Monnet V., Narid M., Chopin A.-C., Gripon J.-C.;
Blochemical and genetic characterization of PepF, an oligopeptidase from Lactococcus lactis...;
J. Biol. Chem. 269:32070-32076(1994).
                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                              Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris)
p54124; P94880;
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2001 (Rel. 40, Last annotation update)
01igoendopeptidase F, plasmid (EC 3.4.24.-).
                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENÇE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z32522; CAA83534.1; -. EMBL; X99798; CAA68133.1; -.
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284 RYIELRKKILGITDL 298
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                   NCBI_TaxID=1359;
                                                                                                                                                                                                                                        STRAIN-NCDO 763;
                                                                                            PEPF1 OR PEPF.
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Q9CEV7;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ED / KW20 / ATCC 51907;
MEDLINE-9535030; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geognagen N.S.M.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: CONVERTS HOLO-ACP TO APO-ACP BY HYDROLYTIC CLEAVAGE OF THE PHOSPHOPANTETHEINE RESIDUE FROM ACP (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: [Acyl-carrier protein] + H(2)0 - 4'-
phosphopantetheine + apoprotein.
-1- SIMILARITY: BELONGS TO THE ACPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Chandler M.S., Smith R.A., "Characterization of the Haemophilus influenzae topA locus: DNA topoisomerase I is required for genetic competence."; Gene 169:25-31(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1; Length 194;
Pred. No. 3.5;
4; Mismatches 3; Indels
                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
ACYl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP phosphodiesterase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Complete proteome.
SEQUENCE 194 AA; 21208 MW; ABAEC9D00829522C CRC64;
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                                                                                            194 AA
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                              STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-96186898; PubMed-8635745;
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53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U20964; AAC43728.1; -. EMBL; U32816; AAC23013.1; -. TIGR; HI1366; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 QYMKSILGFIGITDV 161
                                                                                            STANDARD;
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   124 QYITSNATFTGLSE 137
                                                                                                                                                                                                                                        Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=727;
                                                                                                                                                                                                                       ACPD OR HI1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
PEF1_LACLC
ID PEF1_LACLC
                                                                                            ACPD_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ID ACPD_HA
ID ACPD_HA
ID ACPD_HA
ID 01-NOV.
DT 01-NOV.
DE ACY1 co
DE ACCD O
OS Haemop
OC Bacter
OC Haemop
OC RECTER
RN 11
RN 11
RN SEQUEN
RX SEGUEN
RX MEDLIN
RX MEDLIN
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COCCARREO

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                                                                                                     "Duplication of the pepf gene and shuffiling of DNA fragments on the lactose plasmid of Lactococcus lactis.";
J. Bacteriol. 179:4164-4171(1997)
-i. FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERIOR INTERIOR INTERIOR INTERIOR INTERIOR INTERIOR PROSTER; PROSTER; PSO0142; ZINC_PROTEASE; FALSE_NEG.
Hydrolase, Metalloprotease; Zinc; Plasmid.
METAL 387 ZINC (CATALYTIC) (BY SIMILARITY).
ACT_SITE 388 388 BY SIMILARITY.
ACT_SITE 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
METAL 394 ZINC (CATALYTIC) (BY SIMILARITY).
METAL 394 ZINC (CATALYTIC) (BY SIMILARITY).
ACT_SITE 518 F -> S (IN REF. 2).
ACT_SITE 518 F -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                ACIDS WITH A RATHER WIDE SPECIFICITY.
-!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.1%; Score 40; DB 1; 46.7%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
011goendopeptidase F homolog (EC 3.4.24.-).
01FF OR LL1727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
STRAIN-NCDO 763;
MEDLINE-97352670; PubMed-9209029;
Nardi M., Renault P., Monnet V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
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Pfam; PF00406; adenylatekinase; 1.
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                                                                                                                                                                                                                                                                       PIR; S46746; S46746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S02851; KIYMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAD_MYCCA
P10251:
                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
VIII.";
Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                         Bolotin A., Wincker P., Marger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus archis ssp. lactis Lil403".

- FONCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO ACIDS WITH A RATHER WIDE SPECIFICITY (BY SIMILARITY).

- COPACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Larteille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Ribes L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; lpr00130; Zn_Pro.

InterPro: IPR000130; Zn_Pro.

R Pfam; PF07432; Peptidase_M2; I.

R PROSTIE; PS00142; Z1NC_PROTEASE; I.

Hydrolase; Metalloprotease; Zinc; Complete proteome.

AN Hydrolase; Metalloprotease; Zinc; Metalloprotease
  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical aldehyde-dehydrogenase like protein in FIL1-VMA10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No
                                                                                                                                                MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006403; AAK05825.1; -.
InterPro; IPR001567; Peptidase_M3.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
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284 RYIELRKKILGITDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 7; Conserv
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                                                                                                          SEQUENCE FROM N.A.
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                                                              NCBI_TaxID-1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHJ9_YEAST
P38694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaudin M.;
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content ign in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelib-sib.ch).
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STRAIN-ATCC 27343 / KID;
STRAIN-ATCC 27343 / KID;
MEDILINE-88142549; Pubmed-3481422;
Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;
Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;
"The ribosomal protein gene cluster of Mycoplasma capricolum.";
Mol. Gen. Genet. 210:314-322(1987).
-!- FUNCTION: THIS SMALL UBIOUTPOUS ENZYME IS ESSENTIAL FOR HAINTENANCE AND CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma capricolum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Entomoplasmataceae.
Science 265:2077-2082(1994).
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MR-1989 (Rel. 10, Created)
1-MR-1989 (Rel. 10, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
16-CT-2001 (Rel. 40, Last annotation update)
16-GT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 644;
Pred. No. 12;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
-i- SUBUNT: MONOMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54DADDAEB2A16D4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS;
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Oxidoreductase. ACT_SITE 354 BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S0001081; YHR039C.
rPro; IPR002086; Aldehyde_dehydr.
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InterPro; IPR000850; Adenylate_kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 389 E
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U00062; AAB68915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.1%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 60.0
Matches 9; Conservative
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DR DR SO.

us-09-787-126-34.rsp

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Job time : 4.76205 secs
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STRAIN-JAL-1, DSM 2661 / ATCC 43067;
STRAIN-JAL-1, DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Scatton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Adams M.D., Richer R., Kirkness E.F., Weinstock K.G., Whrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                         Ouery Match 52.7%; Score 39; DB 1; Length 213; Best Local Similarity 72.7%; Pred. No. 5.9; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.4%; Score 38; DB 1; Length 256; 50.0%; Pred. No. 11; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
HYPOTHETICAL PROTEIN MJ1383.
GD26F427EAB54675 CRC64;
                                                                                     Transferase, Kinase, ATP-binding.

NP_BIND
7 15 ATP (BY SIMILARITY).
SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;
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Interpro: IRR001130; TatD.

Ffam: PF01026; TatD_DNase; 1.

Hypothetical protein; Signal; Complete proteome.

1 30 POTENTIAL: DROTEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ1383 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA.
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                              ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35, Created)
      PR00094; ADENYLTKNASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 E
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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183 YFKTNSKFIEI 193
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256 AA;
                                                                                                                                                                                                                                                                                                                            2 YIKANSKFIGI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2190;
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Q58778;
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PRINTS;
ProDom;
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YD83_METJA
ID YD83_MI
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Matches
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Search completed: October 10, 2002, 16:04:53

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October 10, 2002, 12:48:46; Search time 4.83434 Seconds (without alignments) 536.769 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                        .562222 seqs, 172994929 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                               US-09-787-126-34
74
1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                   Title:
Perfect score:
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                                                                                                                                                                                                                                            Sequence:
                                                                                                                       Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries sp_unclassified:* sp_fung1:*
sp_human:*
sp_invertebrate:* sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_archea:* sp_bacteria:* sp_rodent:* sp_mammal:* sp_plant:* sp_virus:* SPTREMBL_19:* sp_phage:* sp_mhc:* Database :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

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Description	093n27 clostridium 031585 salmo salar 09xrj9 salvelinus 0951s2 salmo salar 095hy1 salmo salar 095hx4 salmo salar	031590 salmo salar 09x37 guillardia 09x37 guillardia 031578 salmo salar 09cf6 lactococcus 09mc17 streptococc 09x198 lactococcus 09cr4 mus musculu 09cr4 ataline her 025961 plasmodium
SUMMARIES	Q93N27 Q31585 Q9XKJ9 Q951X2 Q95HY1 Q95HX4	021590 021578 021578 09CEF6 09MCL/7 09CRV4 09CRV4 09CYD2 09CYD2
. BB	urrrr	7 10 10 11 11 12 12 13
% Duery Match Length DB	1310 60 71 71 85 85 85	244 546 67 180 250 252 302 309 899
å Ouery Match	100.0 60.1 60.1 60.1 60.1 60.1	52888888888888888888888888888888888888
Score	44444 44444 47	4 4 4 4 4 4 4
Result No.	0.54321	7 9 8 8 11 11 11 11 11 11 11 11 11 11 11 11

		Q9tzt4 plasmodium			09dek4	٠	0951r2@salmo salar					0	097hk7	096671	Q9vu53	salmo				,	09dej6	salmo		-	'n	salmo	-	Q95hx9 salmo salar		ALIGNMENTS	
O9NHX1	Q9TZT5	Q9TZT4	025922	024262	Q9DEK4	095183	0951R2	031495	онсэ6о	696369	09рзв9	Q9HD07	Q97HK7	096671	Q9VU53	031577	031581	031582	Q9XRH1	Q9XRH6	Q9DEJ6	095159	095158	981560	095185	Q95HY2	Q95HY0	095HX9		ALIG	
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1694	1694	1704	1720	1333	84	85	82	149	216	216	247	384	447	532	540	67	29	67	71	71	84	95	85	82	82	82	82	85			
57.4	57.4	57.4	57.4	8.95	56.1	. 56.1	56.1	56.1	56.1	56.1	55.4	55.4	55.4	55.4	55.4	54.7	54.7	54.7	54.7	54.7	54.7.	54.7	54.7	54.7	54.7	54.7	54.7	54.7	•		
42.5	42.5	42.5	42.5	42	41.5	41.5	41.5	41.5	41.5	41.5	41	41	41	41	41	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5			
17	18	19	20	21	. 22	23	24	25	26	27	. 78	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45			

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Gaps
                                                                                             TETANUS TOXIN (FRAGMENT).

Clostridium tetani,
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                                                                                                         Length 1310;
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NON_TER 1310 1310
SEQUENCE 1310.AA; 150316 MW; 9EADDC914418E450 CRC64;
                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                       SEQUENCE. FROM N.A.
Shumin Z., Dianliang L.;
"Cloning and sequence analysis of tetanus toxin gene.";
submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF389424; AAK72964.2; -.
                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB.2; I
100.0%; Pred. NO. 0.00014;
ttive 0; Mismatches 0;
                           PRT; 1310 AA.
                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                             NCBI_TaxID-1513;
RESULT 1
Q93N27
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031585 PRELIMINARY; PRT; 60 AA. 031585; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) (DB02) MHC CLASS II BETA 1 (FRAGMENT). RESULT 2 Q31585 qq 224448

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(TrEMBLrel. 19, Created)
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Immunogenetics 53:329-336(2001).
EMBL; AF104370; AAL04002.1; -.
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55.6%;
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Matches 10; Conservative
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SEQUENCE
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095нх4;
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Q95HY1
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                                                                                                                                                                                                                                                                                                  Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
"A study of polymorphism in the MHC class II beta 1 and MHC class I alpha 2 domain exons of Atlantic salmon (Salmo salar).";
submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salvelinus namaycush (lake trout).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
VCBI_TaxID-8040;
Salmo salar (Atlantic salmon).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44.5; DB 7; Length 60;
Pred. No. 1.2;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

DOTSCHNET M.O., Duris T., Phillips R.B.;

Diversity of a Lake Trout Mhc class II Gene.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF130026; AAD20889.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AA; 8002 MW; E3095286582A9F2D CRC64;
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60 AA; 6776 MW; 5D4F3449060940E2 CRC64;
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC CLASS II BETA 1 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1993) to the EMBL/GenE
EMBL: L24953; AAA49597.1; -
INTERPRO: IPRO00353; MHC_II_beta.
Pfam: PF00969; MHC_II_beta: 1.
ProDom; PD000328; MHC_II_beta: 1.
Glycoprotein; MHC_II_transmembrane.
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Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC II; Transmembrane.
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55.6%;
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Pest Local Similarity 55.6%;

atches 10; Conservative
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Best Local Similarity 55.6
Matches 10; Conservative
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NON_TER
SEQUENCE
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Q9XRJ9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Suteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8030;
Salmo salar (Atlantic salmon).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Actinopterygii; Salmoniformes; Salmonidae; Salmo.
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MEDLINE-21383619; PubMed-11491536;
Langefors A., Lohm J., von Schantz T.;
"Allelic polymorphism in MHC class II B in four populations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.5; DB 7; Length 85; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44.5; DB 7; Length 85; Pred. No. 1.7; 2; Indels 3; Mismatches 2; Indels
                                                                                                                                                                        SEQUENCE FROM N.A.

"Landry C., Bernatchez L.;

"Comparative analysis of population structure across envir geographic scales at Major Histocompatibility Complex and microsatellite in Atlantic salmon (Salmo Salar).";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF373699; AAK61882.1;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC CLASS II B ANTIGEN (FRAGMENT).
DB1.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC CLASS II B ANTIGEN (FRAGMENT).
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SEQUENCE FROM N.A.
MEDLINE-20087226; PLDMed-10618395;
Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
Zavaller-Smith T., Maier U., Douglas S.,
"Chloroplast protein and centrosomal genes, a tRNA intron, and odd telomeres in an unusually compact eukaryotic genome, the cryptomonad
                                                                                                                                                                                                                                                                                                                                                   PEDGENCE FROM NA.
MEDLINE-2123149; PubMed-11323671;
MEDLINE-2123149; PubMed-11323671;
MEDLINE-2123149; PubMed-11323671;
MU X., Raith M., Cavalier Smith T., Maier U.;
The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001).
Nature 410:109592; CAR404603.1; -.
Hypothetical protein.
SEQUENCE 546 AA; 66218 MW; 7303950F632BE6F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(DB03) MHC CLASS II BETA 1 (FRAGMENT).
Salmo salar (Atlantic salmon).
Salmo salar (Atlantic salmon).
Actinopterrygii; Neopterrygii; Teleostei; Euteleostei;
Protacanthopterrygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length
                                                                                            Guillardia theta (Cryptomoias phi).
Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TaxID=55529;
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                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 66.2 KDA PROTEIN.
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Pred. No. 14;
6; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43.5; DE Pred. No. 2; 4; Mismatches
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Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC_II; Transmembrane.
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50.0%;
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50.0%;
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InterPro; IPR000353: MHC T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.8
Best Local Similarity 50.0
Matches 9; Conservative
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445 FIKSNSRFMRLTEI 458
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nes 7; Conserv
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Q31578;
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X MEDILINE-93170890; PubMed-8436418;

A HOIGHINE-93170890; PubMed-8436418;

A HOIGHINE-93170890; PubMed-8436418;

Cloning and sequence analysis of CDNAs encoding the MHC class II achain in Atlantic salmon, Salmo salar.";

I minunogenetics 37:437-441(1993).

R EMBL; X70166; CAA49725.1; -...

R INTERPOS I IBMO SALAS IBMC II_Deta.

R INTERPOS I PR003597; Ig_Cl.

R INTERPOS I PR003597; Ig_Cl.

R INTERPOS I PR003597; Ig_Cl.

R Pfam; PF00047; ig; 1.

R Pfam; PF00047; ig; 1.

R Pfam; PF00047; ig: 1.

R PADDOM; PD000328; MHC_II_Deta; 1.

R SMARY; SM00407; IGCl; 1.

R Glycoprotein; MHC II; Transmembrane.
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Salmo salar (Atlantic salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8030;
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                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-21383619; PubMed=11491536;
Langefors A., Lobm J., von Schantz T.;
"Allelic polymorphism in WHC class II B in four populations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.1%; Score 44.5; DB 7; Length 244; 55.6%; Pred. No. 5.1; ive 3; Mismatches 2; Indels
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NON_TER 86 86
SEQUENCE 86 AA; 9912 MW; E5097729F681F149 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                     Atlantic salmon (Salmo salar).";
Immunogenetics 53:329-336(2001).
EMBL; AF104377; AAL04009.1; -.
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55.6%;
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Best Local Similarity 55.69
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Matches 10; Conservative
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Q31590;
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57.18;
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130 QVLKANMKIVGATE 143
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Matches 8; Conserv
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus thermophilus bacteriophage 7201.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxIb=112023;
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                                                                                                                                                                                                                                                                                                                                                                        58.1%; Score 43; DB 16; Length 180; 69.2%; Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF145054; AAF45506.1; -
InterPro; IRR002295; D21N6_mtfrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28744 MW; 725EA3B2B56B0D7F CRC64;
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                                                              (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
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Last annotation update)
                                       180 AA.
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"Identification of four loci isolated from
                                                                                                    SPERMIDINE ACETYLTRANSFERASE (EC 2.3.1.57).
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                         PRT;
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MEDLINE-21235186; PubMed-11337471;
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InterPro; IPR002941; N6_N4_Mtase.
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30 AA; 21022 MW;
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PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21N4MTFRASE.
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                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                         Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                    Transferase;
                                                               01-JUN-2001
01-JUN-2001
01-OCT-2001
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                                       Q9CF66
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               RESULT 10
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Score 43; DB 9; Length 250;

58.1%;

Query Match

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van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F.; "Molecular analysis of the temperate lactococcal phage Tuc2009."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF109074, AMB3103.1; InterPro; IPR002295; D21N6 mifrase. InterPro; IPR001091; N4_MTase.
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                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis bacteriophage Tuc2009. "\
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
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                        Indels
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                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE METHYLASE.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                     252 AA
ed. No. 9.7;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3110030A04RIK PROTEIN (FRAGMENT). 3110030A04RIK.
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PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21N4MTFRASE.
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PROSITE; PS01179; PID; 1. SEQUENCE 309 AA; 35272 MW; 535DDBE733C0F406 CRC64;

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KRAIN-C5/BL/65; TISSUE-EMBRYO;

KRAWA J., Shinaqawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

KRAWA J., Shinaqawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

Arawa K., Isawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,

Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rubil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

Rusonstein M.J., Bult C., Retcher C., Fullita M., Gariboldi M.,

Rusonstein M.J., Bult C., Retcher C., Fullita M., Gariboldi M.,

Rusonstein M.J., Bult C., Redriguez I., Sakamoto N.,

Rosaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshw-Boris A., Yoshida K., Rasegawa Y., Kawaji H., Kohtsuki S.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Rawaji H., Kohtsuki S., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK014093; BAB29151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection.";
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Pred. No. 12;
3; Mismatches 3; Indels
                                                                                                                                                                                MGD; MGI:1920407; 3110030A04Rik.
MGD; MGI:1920407; 3110030A04Rik.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR002086; Aldehyde_dehydr.
Ffam; PF00640; PTD; 1.
SWART; SM00462; PTB; 1.
PROSITE; PS010687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
PROSITE; PS01179; PID; 1.
NON_TER 1 1 1
SEQUENCE 302 AA; 34207 MW; 8CB11440F898C65A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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nterPro; IPR000050; PID_domain.
fam; PF00640; PID; 1.
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57.1%;
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Best Local Similarity 57.1v
-hes 8; Conservative
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22 YIPYNAKFLGSTEV 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 YIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730529006RIK PROTEIN
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Score 43; DB 11; Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-73;
Albrecht J.-C., Fleckenstein B.;
Albrecht G.-C., Fleckenstein B.;
Submitted (AuG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083444 AAC9587.1;
SEOUENCE 899 AA; 103389 MW; 19440A7944DE2531 CRC64;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                         "Primary structure of the Herpesvirus Ateles genome."; J. Virol. 74:1033-1037(2000).
                                                                                                                                                                                                                                                             no RNA stage; Herpesviridae;
                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 12;
Pred. No. 36;
1; Mismatches 4;
                                                                                                                                                          899 AA.
                Pred. No. 12;
3; Mismatches
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                                                                                                                                                           PRT;
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MEDLINE-20091363; PubMed-10623770;
                                                                                                                                                                                                                                                                          Gammaherpesvirinae; 'Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.1%;
Best Local Similarity 64.3%;
Matches' 9; Conservative
Ouery Match 58.1%;
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                              Viruses; dsDNA viruses,
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                                                        2 YIKANSKFIGITEL 15
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24 YIPYNAKFLGSTEV 37
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=85618;
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October 10, 2002, 12:48:46; Search time 1.80723 Seconds (without alignments)
202.732 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                            231628 segs, 24425594 residues
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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74
1 QYIKANSKFIGITEL 15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Issued_Patents_AA:*

Database:

SUMMARIES

Description Sequence DB Query Match Length Result Š

Sequence 10, Appl Sequence 6, Appli Sequence 7, Appli Sequence (Sequence Seq Sequence Sequence Sequence Sequence Sequence S Sequence Sequence Sequence Sequence US-08-488-351A-57 US-08-488-351A-63 US-08-446-692-35 US-08-488-351A-13 PCT-US93-11703-63 JS-08-488-351A-35 US-09-100-409A-40 PCT-US95-08596-23 US-09-248-588-55 US-08-446-692-13

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Gaps

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Length 15; Indels

Query Match 100.0%; Score 74; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.3e-07; Matches 15; Conservative 0; Mismatches 0;

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Appl	Appl	Appl	, App	Appl	Appl	Appl	Appl	, App	, App	Appl	Appl	Appl	Appl	Appl	Appli	Appli	Appli	
95,	22,	31;	110	26,	27,	28,	32,	111	112	13,	14,	13,	14,	29,	6	7,	6	
Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequepce	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	
PCT-US95-02121-95	PCT-US92-07218-25	PCT-US92-07218-31	PCT-US95-02121-110	PCT-US92-07218-26	PCT-US92-07218-27	PCT-US92-07218-28	PCT-US92-07218-32	PCT-US95-02121-111	PCT-US95-02121-112	US-09-075-257A-13	US-09-075-257A-14	US-09-534-639-13	US-09-534-639-14	PCT-US92-07218-29	US-08-186-266-9	US-09-171-969-7	US-08-661-052-9	
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70	70	70	20	7.0	70	70	70	70	70	70	70	70	70	70	70	70	69	
28	53	30	31.	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS '

RESULT 1 155-08-139-704-10 156-08-139-704-10 15 Sequence 10, Application US/08319704 15 Patent No. 5814617 16 GENERAL INFORMATION: 16 APPLICANT: Hedfman, Stephen L. 17 APPLICANT: Charcenvit, Yupin 17 APPLICANT: Hedstrom, Richard C. 17 APPLICANT: Hedstrom, Richard C. 17 APPLICANT: Hedstrom, Richard C. 17 TILE OF INVERTION: Protective 17 kDa Malaria Hepatic 17 TILE OF INVERTION: Protective 17 kDa Malaria Hepatic 17 TILE OF INVERTION: Erythrocytic Stage Immunogen and GORRESPONDENCE ADDRESS: 18 APPLICANT Hedstas: 11 18 CORRESPONDENCE ADDRESS: ADDRESSEE: Naval Medical R & D Command STATE: Maryland COMPUTRY: US.A 2 IP: 20889-5606 COMPUTRY: BEADABLE FORM: COMPUTRY: BEADABLE FORM: COMPUTRY: BAPELICATION DATA: APPLICATION NUMBER: US/08/319,704 FILING DATE: 07-0CT-1994 CILASSIPICATION NUMBER: 24,743 REFERENCE/DOCKET NUMBER: 24,743 REFERENCE/DOCKET NUMBER: 24,743 REFERENCE/TOCKET NUMBER: 24,743
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APPLICANT: Sudhir Paul
APPLICANT: Larry J. Smith
APPLICANT: Larry J. Smith
APPLICANT: Gennady GOLOLObov
TITLE OF INVENTION: Methods for Identifying Inducers and
TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their
TITLE OF INVENTION: Use
FILE REPERENCE: UNMC 63123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
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                                                                                             SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
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Pred. No. 1.3e-07;
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CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                   US/08/460,502
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Patent No. 6270765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09046373 Patent No. 6235714 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GOLITCK, MARY E.
REGISTRATION NUMBER: 327,
REFERENCE/COCKET NUMBER: 227,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 221-8458
TELEPHONE: (216) 221-0816
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOCOMPANDED OF THE SYSTEM SYS
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Joel Goldstein
Robert Graziano
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US-09-046-373-2
                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QYIKANSKFIGITEL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                         CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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Patent No. 5843464
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Raumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEQUENCES: 11.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 74; 100.0%; Pred. No. 1
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APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATONNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  Sequence 6, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
                                                                                                                                                                                                                      APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617)227-5941
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SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE: internal
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                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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atches 15; Conserv
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TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
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APPLICANT: Birkett, Ashley J.
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and TITLE OF INVENTION: their Derivatives
FILE OF INVENTION: their Derivatives
FILE REPERENCE: SYN-101 4564/69529
CURRENT FILING DATE: 1999-102-11
EARLIER APPLICATION NUMBER: 60/074537
EARLIER FILING DATE: 1998-02-12
NUMBER OF SEO ID NOS: 113
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 55
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                Length 15;
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100.0%; Score 74; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                Score 74; DB 5;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                 0222.101
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Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                        31,259
                                                                                                                                                                                                                                                                                                                                                   100.0%;
ATTORNEY/AGENT INFORMATION: NAME: Green, Grant D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Clostridium tetani
                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 15; Confervative
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                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide PCT-US93-11703-69
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CORRESPONDENCE ADDRESS:
                                      REGISTRATION NUMBER:
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                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-248-588-55
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  Chezian Somasundaram
VENTION: THERAPEUTIC COMPOUNDS COMPRISED
                                               OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
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SEMERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFRENCE/DOCKER NUMBER: MXI-043CP
FELECOMMUNICATION: INFORMATION:
                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/661,052
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617)227-5941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)227-594 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FRAGMENT TYPE: internal
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                                                                                                                                                                           Massachusetts
                                                                 NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
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                        ITLE OF INVENTION:
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                                                                                                                                                                                                               02109-1875
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                                                                                                                                                       Boston
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US-09-100-409A-40

US-09-100-409A-40

Sequence 40, Application US/09100409A

Sequence 40, Application US/09100409A

Sequence 40, Application US/09100409A

Fatent No. 609038B

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: PREPETIDE COMPOSITION FOR

TITLE OF INVENTION: IMMUNE DISORDERS

TITLE OF INVENTION: IMMUNE DISORDERS

WUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
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Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 74; DB 2; Best Local Similarity 100.0%; Pred. No. 1.5e-07; Matches 15; Conservative 0; Mismatches 0;
                                          ATTING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: Maria C.H. Lin
RAGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/100,409A
          RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bub PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 40:
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                             LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECQUE TYPE: peptide
US-08-488-351A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-09-100-409A-40
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Best Local Similarity
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APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: A PACHICIN Release #1.0, Version #1.25

SOFTWARE: PACHICIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995
                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
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Pred. No. 1.5e-07;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
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14-APR-1994
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                                                                                                                                                                                                                                                                  FILING DATE: 7-JUN-1995
CIASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTATION UNDHER: 29, 323
REFERENCE/COCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
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100.0%;
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345 Park Avenue
3: Maria C.H. Lin
345 Park Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nes 15; Conservative
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APPLICATION NUMBER: [
FILING DATE: 14-APR-]
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                                          New York
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  ADDRESSEE:
STREET: 34
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Gaps

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TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 345 Park Avenue
CITY: New York
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NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,3
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APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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Best Local Similarity 100.
Matches 15; Conservative
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CLASSIFICATION:
               USA
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STATE:
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APPLICANT: Wang, Chang Yi
TILLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
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 Indels
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and Treating Type I Diabetes
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 Mismatches
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08596
                                                                                                                                                                                              APPLICANT:
TITLE OF INVENTION: Proinsulin Peptic
TITLE OF INVENTION: and Treating Type
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ALBURESS:
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,220
FILING DATE: 08-JULX-1994
CLASSIFICATION:
                                                                                                                                                              Sequence 23, Application PC/TUS9508596 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application PC/TUS9513841 GENERAL INFORMATION:
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345 Park Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
15; Conservative
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                                   1 QYIKANSKFIGITEL 15
                                                      3 QYIKANSKFIGITEL 17
                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
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PCT-US95-13841-7
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 Matches
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                                                          OFFWARE: WORDFELLUCTORY
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13841
                                                                                                                                                                      08/328,519
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                                                                                                                                                                                                                                  NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3:
FILING DATE: 25-OCT-1994
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NAME: Lin, Maria C.H.
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Length 27;
                                         Indels
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  Score 74; DB 2; Pred. No. 2.5e-07;
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                                                                                                                                                                                                                                                            APPLICANT: Chiron Mimotopes Pty. Ltd
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTONBY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
                                                                                                                                                                                                        Sequence 63. Application PC/TUS9311703 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%;
ilarity 100.0%;
Conservative 0
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STREET: 4560 Horton St.
CITY: Emeryvi‡le
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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linear
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                                                                                                      3 OYIKANSKFIGITEL 17
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STRANDEDNESS: si
    Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: USI
ZIP: 94608
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                                                                                                                                                                                                        PCT-US93-11703-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RH peptide constructs
universal immune stimulators for vaccines
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                          Query Match 100.0%; Score 74; DB 1; Best Local Similarity 100.0%; Pred. No. 2.5e-07; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
PELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PELICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSTRICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSTRICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION UNMBER: US 08/229,275
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/057,166
TTING DATE: 27-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-488-351A-13
"Requence 13, Application US/08488351A
atent No. 5843446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: and synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Maria C.H. Lin
1: 345 Park Avenue
New York
          (212)415-8745
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LENGTH: 27 amino acids
                                                                                                  ; TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H
STREET: 345 Park Ave.
                                                                                                                                                                                                                                                                                           1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                DD -- 3 QYIKANSKFIGITEL 17
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            TELEPHONE:
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